

(TM)

protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:11:52 1999: MacPort time 0.35 seconds

Tabular output not generated.

Title: >US-08-477-989B-88  
Description: (1-112) from US08477989B, pep  
perfect score. 810

Sequence: 1 DVVMTQSPPSLLVLGPAS.....CMQTHYPYTFGGGTKLEIK 112

Scoring table: PAM 150  
Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p1r58

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 40.865; Variance 103.061; scale 0.397

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query		Length	DB	ID	Description	Pred. No.
	Score	Match					
1	673	83.1	131	2	S31577	Ig kappa chain - mous	5.35e-87
2	659	81.4	112	2	PL0273	Ig kappa chain v regi	1.00e-84
3	653	80.6	142	2	S22902	Ig kappa chain v regi	9.42e-84
4	648	80.0	113	2	F30560	Ig kappa chain v regi	6.09e-83
5	647	79.9	133	2	S32330	Ig kappa chain precu	8.84e-83
6	646	79.8	112	2	A55491	protoclytic antibody	1.28e-82
7	646	79.8	132	2	C32513	Ig kappa chain precu	1.28e-82
8	637	78.6	112	2	A36259	Ig kappa chain v regi	3.68e-81
9	636	78.5	140	2	S22658	Ig kappa chain precu	5.35e-81
10	635	78.4	114	2	S49572	Ig kappa chain precu	7.76e-81
11	634	78.3	126	2	A40312	Ig kappa chain - huma	1.13e-80
12	633	78.1	133	1	K2H0NP	Ig kappa chain precu	1.64e-80
13	632	78.0	112	2	B49060	Ig light chain v regi	2.37e-80
14	631	77.9	111	2	S20709	Ig kappa chain v regi	3.44e-80
15	630	77.8	103	2	PH1056	Ig light chain v regi	5.00e-80
16	630	77.8	112	2	A26317	Ig kappa chain v regi	5.00e-80
17	628	77.5	112	2	G26317	Ig kappa chain v regi	1.05e-79
18	625	77.2	112	2	F26317	Ig kappa chain v regi	3.22e-79
19	625	77.2	113	1	KVMST5	Ig kappa chain v regi	3.22e-79
20	625	77.2	118	2	S40374	Ig kappa chain - huma	3.22e-79
21	623	76.9	112	2	B26317	Ig kappa chain v regi	6.77e-79
22	621	76.7	112	2	E26317	Ig kappa chain v regi	1.43e-78
23	621	76.7	133	1	A24452	Ig kappa chain precu	1.43e-78

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#cross-references MUID:90111618
#accession F30560
#molecule_type mRNA
#residues 1-112 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-23 #region framework 1\
24-39 #region complementarity-determining 1\
40-54 #region framework 2\
55-61 #region complementarity-determining 2\
62-93 #region framework 3\
94-102 #region complementarity-determining 3\
103-112 #region framework 4\
SUMMARY
length 112 #checksum 8934
Query Match 81.4%; Score 659; DB 2; Length 112;
Best Local Similarity 81.3%; Pred. No. 1.00e-84;
Matches 91; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Db 1 DVNMTQPLTSLVITIGOPASISCKSSQSLVYNGKTYLNWLLQRPQSPKRLIYLVSKLD 60
QY 1 DVNMTQSPPLVTLGQPASISCKSSQSLVYNGKTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 61 SGVPDRFTGSGGDTFLTKISRVAEDLGVIYVYQGTHTFPFTFGGKTLEIK 112
QY 61 SGVPDRFSGSGGDTFLTKISGVAEDGVYVYCMQFTHYPTFGGKTLEIK 112

RESULT 3
ENTRY S22902 #type complete
TITLE Ig kappa chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
ACCESSIONS S22902
REFERENCE S22902
#authors Chastagner, P.; These, J.; Zouali, M.
#journal Gene (1991) 101:305-306
#title Cloning of a gene encoding a lupus-associated human
autoantibody V(K) region using the polymerase chain
reaction and degenerate primers.
#cross-references MUID:91276289
#accession S22902
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-142 #label CHA
#cross-references EMBL:X56510
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 142 #molecular-weight 15579 #checksum 227

Query Match 80.6%; Score 653; DB 2; Length 142;
Best Local Similarity 84.7%; Pred. No. 9.42e-84;
Matches 94; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Db 32 DVNMTQSPPLVTLGQPASISCKSSQSLVHSDGNTYLNWLLQRPQSPKRLIYKVSNRD 91
QY 1 DVNMTQSPPLVTLGQPASISCKSSQSLVHSDGNTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 92 SGVPDRFSGSGGDTFLTKISRVAEDGVYVYCMQGTHTFPFTFGGKTLEI 142
QY 61 SGVPDRFSGSGGDTFLTKISGVAEDGVYVYCMQFTHYPTFGGKTLEI 111

RESULT 4
ENTRY F30560 #type fragment
TITLE Ig kappa chain V region (28.4.10A) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change
20-Mar-1998
ACCESSIONS F30560
REFERENCE A30560

#cross-references MUID:90111062
#accession F30560
#molecule_type preliminary
#residues 1-113 #label MAT
#cross-references GB:M24273; NID:g197081; PID:g197082
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 113 #checksum 1877

Query Match 80.0%; Score 648; DB 2; Length 113;
Best Local Similarity 82.1%; Pred. No. 6.09e-83;
Matches 92; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Db 1 DVNMTQPLTSLVITIGOPASISCKSSQSLVSDGKTYLNWLLQRPQSPKRLIYLVSKLD 60
QY 1 DVNMTQSPPLVTLGQPASISCKSSQSLVSDGKTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 61 SGVPDRFTGSGGDTFLTKISRVAEDLGVIYVYCMQGTHTFPFTFGGKTLEIK 112
QY 61 SGVPDRFSGSGGDTFLTKISGVAEDGVYVYCMQFTHYPTFGGKTLEIK 112

RESULT 5
ENTRY S23230 #type fragment
TITLE Ig kappa chain precursor V-J region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
08-Sep-1997
ACCESSIONS S23230
REFERENCE S23230
#authors Kennedy, M.A.
#journal J. Exp. Med. (1991) 173:1033-1036
#title Novel chromosome translocation caused by fusion of
immunoglobulin heavy and light chain V genes in a human B
lymphoblastoid cell line.
#accession S23230
#status preliminary
#molecule_type DNA
#residues 1-133 #label KEN
#cross-references EMBL:X55400; NID:g33999; PID:g34000
GENETICS
#introns 17/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 133 #checksum 2932

Query Match 79.9%; Score 647; DB 2; Length 133;
Best Local Similarity 84.8%; Pred. No. 8.84e-83;
Matches 95; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Db 21 DVNMTQSPPLVTLGQPASISCKSSQSLVSDGNTYLNWLLQRPQSPKRLIYKVSNRD 80
QY 1 DVNMTQSPPLVTLGQPASISCKSSQSLVSDGNTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 81 SGVPDRFSGSGGDTFLTKISRVAEDGVYVYCMQGTHTFPFTFGGKTLEIK 132
QY 61 SGVPDRFSGSGGDTFLTKISGVAEDGVYVYCMQFTHYPTFGGKTLEIK 112

RESULT 6
ENTRY A55491 #type complete
TITLE proteolytic antibody light chain - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change
03-May-1996
ACCESSIONS A55491

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[illegible]

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9
RESULT
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#accession
#molecule_type
#residues
#cross-references
CLASSIFICATION
KEYWORDS
FEATURE
1-19
20-140
SUMMARY

S22658
Ig kappa chain precursor V region (O-81VL) - human (fragment)
#type fragment
#formal_name Homo sapiens #common_name man
29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change
06-Feb-1998

S22658
Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. (1992) 20:2601
Variable regions of a human anti-DNA antibody O-81 possessing
lupus nephritis-associated idiotype.
S22658

#molecule_type mRNA
#residues 1-140 #label HIR
#cross-references EMBL:X59135
superfamily immunoglobulin V region; immunoglobulin homology
heterotetramer; immunoglobulin

#domain signal sequence #status predicted #label SIG\
#product Ig kappa chain (fragment) #status predicted
#label MAT

#length 140 #checksum 5056

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	Query Match	Best Local Matches	Similarity	Conservative	Score	Pred. NO.	Length	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415
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RESULT	10
ENTRY	
TITLE	S49572 #type fragment
ORGANISM	ig kappa chain precursor - human (fragment)
DATE	#formal_name Homo sapiens - common_name man
	06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change
	20-Mar-1998
ACCESSIONS	S49572
REFERENCE	S49571
#authors	Giachino, C.; padovan, E.; Lanzavecchia, A.
#submission	submitted to the EMBL Data Library, November 1994

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#description k+1+ dual receptor B cells are present in the human
#accession S49572
##status preliminary
##molecule_type mRNA
##molecule 1-114 #label GIA
##residues 1-114 #label GIA
##cross-references EMBL:246626; NID:g575261; PID:g575262
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 114 #checksum 9334

Query Match 78.4%; Score 635; DB 2; Length 114;
Best Local Similarity 82.3%; Pred. No. 7,76e-81;
Matches 93; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

Db 1 DVWMTQSPVLTIGQPASISCRSSQSLVSDGNTYLNWFOQRPGQSPRLIYKVSNRD 60
QY 1 DVWMTQSPVLTIGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60
Db 61 SGVDPFRFSGSGGDTFTLKISVEAEDGVYICMGTHWTFGGQTKLEIK 113
QY 61 SGVDPFRFSGSGGDTFTLKISVEAEDGVYICMGTHWTFGGQTKLEIK 112

RESULT 11
ENTRY S40312 #type complete
TITLE Ig kappa chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
08-Sep-1997
ACCESSIONS S40312
REFERENCE Klein, R.; Jaenichen, R.; Zachau, H.G.
#authors Eur. J. Immunol. (1993) 23:3248-3271
#journal Expressed human immunoglobulin chi genes and their
#title hypermutation.
#accession S40312
#status preliminary; translation not shown
##molecule_type mRNA
##molecule 1-126 #label KLE
##residues 1-126 #label KLE
##cross-references EMBL:X72422; NID:g441312; PID:g441313
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 126 #molecular-weight 13744 #checksum 4861

Query Match 78.3%; Score 634; DB 2; Length 126;
Best Local Similarity 80.4%; Pred. No. 1,13e-80;
Matches 90; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Db 14 DVWMTQSPVLTIGQPASISCRSSQSLVSDGNTYLNWFOQRPGQSPRLIYKISNR 73
QY 1 DVWMTQSPVLTIGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60
Db 74 SGVDPFRFSGSGGDTFTLKISVEAEDGVYICMGTHWTFGGQTKLEIK 125
QY 61 SGVDPFRFSGSGGDTFTLKISVEAEDGVYICMGTHWTFGGQTKLEIK 112

RESULT 12
ENTRY K2HURP #type complete
TITLE Ig kappa chain precursor V-II region (RPMI) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
15-Aug-1997
ACCESSIONS A01890
REFERENCE Kloeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.;
#authors Zachau, H.G.
#journal Nucleic Acids Res. (1985) 13:6499-6513
#title Human immunoglobulin kappa light chain genes of subgroups II
and III
#cross-references MUID:86041852
#accession A01890
##molecule_type DNA

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##residues 1-133 #label KLO
##note the sequence was determined from the differentiated gene
GENETICS
#gene GDB:IGKV2
##cross-references GDB:136265
#map_position 2p12-2p12
#introns 17/1
COMPLEX An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
#superfamily immunoglobulin V region; immunoglobulin homology
heterotetramer; immunoglobulin
CLASSIFICATION
KEYWORDS #domain signal sequence #status predicted #label SIG\
FEATURE #product Ig kappa chain V-II region (RPMI) #status
1-20 predicted #label MAT\
21-133 #region framework 1\
36-115 #domain immunoglobulin homology #label IMM\
44-59 #region complementarity-determining 1\
60-74 #region framework 2\
75-81 #region complementarity-determining 2\
82-113 #region framework 3\
114-122 #region complementarity-determining 3\
123-133 #region framework 4\
43-113 #disulfide-bonds #status predicted
SUMMARY #length 133 #molecular-weight 14707 #checksum 4055

Query Match 78.1%; Score 633; DB 1; Length 133;
Best Local Similarity 83.0%; Pred. No. 1,64e-80;
Matches 93; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Db 21 DVWMTQSPVLTIGQPASISCRSSQSLVSDGNTYLNWFOQRPGQSPRLIYKVSNRD 80
QY 1 DVWMTQSPVLTIGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60
Db 81 SGVDPFRFSGSGGDTFTLKISVEAEDGVYICMGTHWTFGGQTKVEIK 132
QY 61 SGVDPFRFSGSGGDTFTLKISVEAEDGVYICMGTHWTFGGQTKLEIK 112

RESULT 13
ENTRY B49060 #type fragment
TITLE Ig light chain V region, phenyl phosphonate hapten-specific
catalytic monoclonal antibody (isobzyme) 20G9 - mouse
(fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
16-Aug-1996
ACCESSIONS B49060
REFERENCE Angeles, T.S.; Smith, R.G.; Darsley, M.J.; Sugawara, R.;
#authors Sanchez, R.I.; Kenten, J.; Schultz, P.G.; Martin, M.T.
#journal Biochemistry (1993) 32:12128-12135
#title Isozymes: structurally and mechanistically similar
catalytic antibodies from the same immunization.
#cross-references MUID:94032348
#accession B49060
#status preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-112 #label ANG
##experimental_source hybridoma cell
#note sequence extracted from NCBI backbone (NCBIP:140373)
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 112 #checksum 1098

Query Match 78.0%; Score 632; DB 2; Length 112;
Best Local Similarity 75.9%; Pred. No. 2,37e-80;
Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

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Db 1 EIVLTQSPPSVIVTGPESVTSICRSKSLHSGNTYLYWFLQRPQSPQVLIYRMSNLA 60  
 QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQVLIYVSKLE 60  
 Db 61 SGVPDRFSGSGGTFTLRSIRVEADGVVYICQYLEIPYTFGGGKLEIK 112  
 QY 61 SGVPDRFSGSGGTFTLKISGVEADGVVYICQFTHPYTFGGGKLEIK 112

RESULT 14  
 ENTRY TITLE  
 ORGANISM #type complete  
 DATE 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change  
 ACCESSIONS S20709  
 REFERENCE S20706  
 #authors Brennaand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.;  
 Harris, W.J.; Carr, F.J.; Osborn, N.J.; Glennie, M.J.;  
 Richards, N.G.; Robinson, J.A.  
 #submission Submitted to the EMBL Data Library, April 1992  
 #description Binding specificity and variable region sequences of two  
 monoclonal antibodies that recognise a beta-turn forming  
 peptide containing alpha-methylproline.  
 #accession S20709  
 #status preliminary  
 #molecule\_type DNA  
 #residues 1-111 #label BRE  
 #cross-references EMBL:211917; NID:G52655; PID:G52656  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS heterotetramer; immunoglobulin  
 SUMMARY #length 111 #molecular-weight 12122 #checksum 3705

Query Match 77.9%; Score 631; DB 2; Length 111;  
 Best Local Similarity 81.1%; Pred. No. 3.44e-80;  
 Matches 90; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
 Db 1 DIQLTQSPPLSVITIGQPASISCRSSQSLHSGNTYLNWLLQRPQSPKRLIYVSKLD 60  
 QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQVLIYVSKLE 60  
 Db 61 SGVPDRFSGSGGTFTLKISRVEADLVVYICQGHFPTFGGKLEI 111  
 QY 61 SGVPDRFSGSGGTFTLKISGVEADGVVYICQFTHPYTFGGGKLEI 111

RESULT 15  
 ENTRY TITLE  
 ORGANISM #type fragment  
 DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change  
 ACCESSIONS PH1056  
 REFERENCE PH0971  
 #authors Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 #journal J. Exp. Med. (1992) 176:761-779  
 #title Both IgM and IgG anti-DNA antibodies are the products of  
 clonally selective B cell stimulation in (NZB x NZW)F1  
 mice.  
 #accession PH1056  
 #status nucleic acid sequence not shown  
 #molecule\_type mRNA  
 #residues 1-103 #label TIL  
 #experimental\_source B cell, strain [NZB x NZW]F1  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS immunoglobulin  
 SUMMARY #length 103 #checksum 3621

Query Match 77.8%; Score 630; DB 2; Length 103;  
 Best Local Similarity 83.5%; Pred. No. 5.00e-80;  
 Matches 86; Conservative 10; Mismatches 7; Indels 0; Gaps 0;  
 Db 1 DVVMTQSPPLSVITIGQPASISCRSSQSLHSGNTYLNWLLQRPQSPKRLIYVSKLE 60

QY 1 DVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQVLIYVSKLE 60  
 Db 61 SGVPDRFSGSGGTFTLKISRVEADLVVYICQGHFPTFGGKLEI 103  
 QY 61 SGVPDRFSGSGGTFTLKISGVEADGVVYICQFTHPYTF 103

Search completed: Thu Jan 14 17:12:05 1999  
 Job time : 13 secs.

\*\*\*\*\*  
 WQERH  
 \*\*\*\*\*  
 (TM)

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mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:10:34 1999; Maspar time 6.92 Seconds  
 434.138 Million cell updates/sec

Tabular output not generated.

Title: >US-08-477-989B-88  
 Description: (1-112) from US08477989B.pep  
 Perfect Score: 810  
 Sequence: 1 DVVMTOSPPSLVTLGPAS.....CMQFTHYPYTFGGQTKLEIK 112

Scoring table: PAM 150  
 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 04  
 Listing first 45 summaries

Database: swiss-prot35  
 1:swissprot

Statistics: Mean 41.116; Variance 69.429; scale 0.592

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	633	78.1	133	1	KV2F_HUMAN	IG KAPPA CHAIN PRECURS 1.99e-121
2	625	77.2	113	1	KV2F_MOUSE	IG KAPPA CHAIN V-II RE 1.69e-119
3	613	75.7	113	1	KV2E_HUMAN	IG KAPPA CHAIN V-II RE 1.32e-116
4	602	74.3	113	1	KV2D_HUMAN	IG KAPPA CHAIN V-II RE 1.32e-114
5	595	73.5	117	1	KV2E_HUMAN	IG KAPPA CHAIN PRECURS 2.80e-112
6	590	72.8	115	1	KV2A_HUMAN	IG KAPPA CHAIN V-II RE 4.44e-111
7	571	70.5	112	1	KV2C_HUMAN	IG KAPPA CHAIN V-II RE 1.60e-106
8	568	70.1	113	1	KV2G_MOUSE	IG KAPPA CHAIN V-II RE 8.36e-106
9	558	68.9	113	1	KV2E_MOUSE	IG KAPPA CHAIN V-II RE 2.06e-103
10	552	68.1	112	1	KV2D_MOUSE	IG KAPPA CHAIN V-II RE 5.60e-102
11	541	66.8	114	1	KV4A_HUMAN	IG KAPPA CHAIN V-IV RE 2.37e-99
12	534	65.9	134	1	KV4C_HUMAN	IG KAPPA CHAIN PRECURS 1.10e-97
13	514	63.5	112	1	KV2A_MOUSE	IG KAPPA CHAIN V-II RE 6.32e-93
14	512	63.2	113	1	KV2C_MOUSE	IG KAPPA CHAIN V-II RE 1.89e-92
15	510	63.0	111	1	KV3J_MOUSE	IG KAPPA CHAIN V-III RE 5.63e-92
16	510	63.0	133	1	KV4B_HUMAN	IG KAPPA CHAIN PRECURS 5.63e-92
17	508	62.7	111	1	KV3L_MOUSE	IG KAPPA CHAIN V-III R 1.68e-91
18	507	62.6	111	1	KV3M_MOUSE	IG KAPPA CHAIN V-III R 2.90e-91
19	506	62.5	111	1	KV3N_MOUSE	IG KAPPA CHAIN V-III R 5.01e-91
20	504	62.2	111	1	KV3U_MOUSE	IG KAPPA CHAIN V-III R 1.49e-90
21	501	61.9	111	1	KV3S_MOUSE	IG KAPPA CHAIN V-III R 7.68e-90
22	500	61.7	111	1	KV3R_MOUSE	IG KAPPA CHAIN V-III R 1.33e-89
23	499	61.6	111	1	KV3Q_MOUSE	IG KAPPA CHAIN V-III R 2.29e-89

24	498	61.5	110	1	KV3P_MOUSE	IG KAPPA CHAIN V-III R 3.95e-89
25	498	61.5	131	1	KV3I_MOUSE	IG KAPPA CHAIN PRECURS 3.95e-89
26	495	61.1	111	1	KV3Q_MOUSE	IG KAPPA CHAIN V-III R 2.03e-88
27	495	61.1	132	1	KV3F_MOUSE	IG KAPPA CHAIN PRECURS 2.03e-88
28	494	61.0	112	1	KV3G_MOUSE	IG KAPPA CHAIN V-III R 3.50e-88
29	492	60.7	111	1	KV3K_MOUSE	IG KAPPA CHAIN V-III R 1.04e-87
30	492	60.7	111	1	KV3N_MOUSE	IG KAPPA CHAIN V-III R 1.04e-87
31	487	60.1	111	1	KV3T_MOUSE	IG KAPPA CHAIN V-III R 1.58e-86
32	481	59.4	120	1	KV2B_MOUSE	IG KAPPA CHAIN PRECURS 4.15e-85
33	478	59.0	108	1	KV1_CANFA	IG KAPPA CHAIN V REGIO 2.12e-84
34	475	58.6	111	1	KV3C_MOUSE	IG KAPPA CHAIN V-III R 1.08e-83
35	470	58.0	111	1	KV3D_MOUSE	IG KAPPA CHAIN V-III R 1.63e-82
36	468	57.8	112	1	KV3B_MOUSE	IG KAPPA CHAIN V-III R 4.84e-82
37	467	57.7	111	1	KV3A_MOUSE	IG KAPPA CHAIN V-III R 8.32e-82
38	460	56.8	121	1	KV4O_HUMAN	IG KAPPA CHAIN PRECURS 3.70e-80
39	459	56.7	108	1	KV3A_HUMAN	IG KAPPA CHAIN V-III R 6.35e-80
40	450	55.6	108	1	KV3V_MOUSE	IG KAPPA CHAIN V-III R 8.28e-78
41	435	53.7	128	1	KV5E_MOUSE	IG KAPPA CHAIN PRECURS 2.71e-74
42	431	53.2	114	1	KV1L_MOUSE	IG KAPPA CHAIN V-I REG 2.34e-73
43	429	53.0	108	1	KV1L_HUMAN	IG KAPPA CHAIN V-I REG 6.86e-73
44	428	52.8	109	1	KV3F_HUMAN	IG KAPPA CHAIN V-III R 1.17e-72
45	426	52.6	129	1	KV3M_HUMAN	IG KAPPA CHAIN PRECURS 3.44e-72

ALIGNMENTS

RESULT 1						
ID	KV2F_HUMAN	STANDARD;	PRT;	133	AA.	
AC	P06310;					
DT	01-JAN-1988 (REL. 06, CREATED)					
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)					
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)					
DE	IG KAPPA CHAIN PRECURSOR V-II REGION (RPMI 6410).					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 86041852.					
RA	KLOBECK H.G., MEINDL A., COMBIATO G., SOLOMON A., ZACHAU H.G.;					
RL	NUCLEIC ACIDS RES. 13:6499-6513(1985).					
DR	EMBL; Z00020; G296655;					
DR	PIR; A01890; K2HURP.					
DR	HSSP; P01607; 4FAB.					
KW	IMMUNOGLOBULIN V REGION; SIGNAL.					
FT	SIGNAL	1	20			
FT	CHAIN	21	133			
FT	DOMAIN	21	43			
FT	DOMAIN	44	59			
FT	DOMAIN	60	74			
FT	DOMAIN	75	81			
FT	DOMAIN	82	113			
FT	DOMAIN	114	122			
FT	DOMAIN	123	132			
FT	DISULFID	43	113			
FT	NON TER	133	133			
SQ	SEQUENCE	133	AA;	14707	MM;	2DC342B5 CRC32;
Query Match 78.1%; Score 633; DB 1; Length 133;						
Best Local Similarity 83.0%; Pred. No. 1.99e-121;						
Matches 93; Conservative 7; Mismatches 12; Indels 0; Gaps 0;						
Db	21	DVMTOSPLSLVTLGPASISCRSSQSLVSDGNTVLNWFQORPGOSPRLLIYKVSNRD	80			
QY	1	DVMTOSPPSLVTLGPASISCRSSQSLHSSGNTVLNWLQRPQSPQSLIYLVSKLE	60			
Db	81	SGVDFRFGSGSGTDFTLKISRYEAEADVGVYCMQFTHYPYTFGGQTKLEIK	132			
QY	61	SGVDFRFGSGSGTDFTLKISRYEAEADVGVYCMQFTHYPYTFGGQTKLEIK	112			
RESULT 2						
ID	KV2F_MOUSE	STANDARD;	PRT;	113	AA.	

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Query Match      75.7%; Score 613; DB 1; Length 113;
Best Local Similarity 75.9%; Pred. No. 1.32e-116;
Matches      85; Conservative    12; Mismatches   15; Indels     0; Gaps       0;

Db          1 DVMVTOSPLFLPVLCEPASIQCRSSQSLVYRBGBYLWBWLYKPKQGCSPELLIYLSSYRD 60
            | ||||| | | ||||| : ||||| : ||||| : ||||| : ||||| : 
QY         1 DVMYTOSPSPLLVLTGPASISICRSSLHSGSNTYLNWLLQRPGSQPOLIYLVSKLE 60
            | ||||| | | ||||| : ||||| : ||||| : ||||| : ||||| : 

Db          61 SGVPDRFDSGGSTDTFLATIRVQAEDVGYYCMQATZSPYTFGQGTKLZIK 112
            | ||||| | | ||||| : ||||| : ||||| : ||||| : ||||| : 
QY         61 SGVPDRFDSGGSTDTFLKISGVEADVGYCYMQFTHYPTFGQGTKEIK 112
            | ||||| | | ||||| : ||||| : ||||| : ||||| : ||||| : 

RESULT      4
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (REL. 01, CREATED)
DD 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (TEW).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE; 74148480.
RA PUTNAM F.W., WHITLEY E.J. JR., PAUL C., DAVIDSON J.N.;
RL BIOCHEMISTRY 12:3763-3780(1973).
```

14] SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).  
RP MEDLINE: 73166638.  
RX TERRY W.D., PAGE D.L., KIMURA S., ISOBE T., OSSERMAN E.F.,  
RA GLENNER G.G.;  
RL J. CLIN. INVEST. 52:1276-1281(1973).  
RC -!- THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENGE  
CC JONES PROTEIN ISOLATED FROM THE SAME PATIENT.  
CC -!- THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH  
CC PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.  
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
DR PIR: A01888: K2HUTW

[illegible]

IG KAPPA CHAIN PRECURSOR V-II REGION (GM607) (FRAGMENT).

OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE; 84191506.  
 RX KLOBECK H.G., SOLOMON A., ZACHAU H.G.;  
 RL NATURE 309:73-76(1984).  
 DR EMBL; Z00009; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A01889; K2HUGM.  
 DR HSP; P01679; ICBV.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 1  
 FT CHAIN <1 4  
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION (GM607).  
 FT DOMAIN 5 27 FRAMEWORK 1.  
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 44 58 FRAMEWORK 2.  
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 66 97 FRAMEWORK 3.  
 FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 107 116 FRAMEWORK 4.  
 FT DISULFID 27 97 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12664 MW; E09E9ACC CRC32;

Query Match 73.5%; Score 595; DB 1; Length 117;  
 Best Local Similarity 78.6%; Pred. No. 2.80e-112;  
 Matches 88; Conservative 8; Mismatches 16; Indels 0; Gaps 0;  
 Db 5 DIVMTQSPSLPVTGPGSPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKLE 64  
 QY 1 DVMTQSPSLPVTGPGSPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKLE 60  
 Db 65 SGVPDRFSGSGGTDFTLKISRVAEDVGVYCMQGLQTPTFGGQTKLEIK 116  
 QY 61 SGVPDRFSGSGGTDFTLKISRVAEDVGVYCMQGLQTPTFGGQTKLEIK 112

RESULT 6  
 ID KV2A\_HUMAN STANDARD; PRT; 115 AA.  
 AC P01614;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (CUM).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 68242259.  
 RA HILSCHMANN N.;  
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 348:1718-1722(1967).  
 RN [2]  
 RP REVISIONS TO 50; 52; 96 AND 97.  
 RX MEDLINE; 70063440.  
 RA HILSCHMANN N.;  
 RL NATURWISSENSCHAFTEN 56:195-205(1969).  
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01885; K2HUGM.  
 DR HSP; P01607; IIGI.  
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.  
 FT DISULFID 24 95 BY SIMILARITY.  
 FT NON\_TER 115 115  
 SQ SEQUENCE 115 AA; 12676 MW; 5500220A CRC32;

Query Match 72.8%; Score 590; DB 1; Length 115;  
 Best Local Similarity 77.9%; Pred. No. 4.44e-111;  
 Matches 88; Conservative 9; Mismatches 15; Indels 1; Gaps 1;  
 Db 2 DIVMTQSPSLPVTGPGSPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKLE 61

QY 1 DVMTQSPSLPVTGPGSPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKLE 59  
 Db 62 ASGVDPDRFSGSGGTDFTLKISRVAEDVGVYCMQGLQTPTFGGQTKLEIK 114  
 QY 60 ESVGDPDRFSGSGGTDFTLKISRVAEDVGVYCMQGLQTPTFGGQTKLEIK 112

RESULT 7  
 ID KV2C\_HUMAN STANDARD; PRT; 112 AA.  
 AC P01616;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (MIL).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE.  
 RA DREYER W.J., GRAY W.R., HOOD L.E.;  
 RL COLD SPRING HARB. SYMP. QUANT. BIOL. 32:353-367(1967).  
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01887; K2HUGM.  
 DR HSP; P01679; ICBV.  
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 39 53 FRAMEWORK 2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 61 92 FRAMEWORK 3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 102 111 FRAMEWORK 4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 12055 MW; C487DFDF CRC32;

Query Match 70.5%; Score 571; DB 1; Length 112;  
 Best Local Similarity 67.9%; Pred. No. 1.60e-106;  
 Matches 76; Conservative 21; Mismatches 14; Indels 1; Gaps 1;  
 Db 1 DIVMTQSPSLPVTGPGSPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKLE 59  
 QY 1 DVMTQSPSLPVTGPGSPASISCRSSQSLHSSGNTYLNWLLQRPQSPOLLYLVSKLE 60  
 Db 60 SGVPDRFSGSGGTDFTLKISRVAEDVGVYCMQGLQTPTFGGQTKLEIK 111  
 QY 61 SGVPDRFSGSGGTDFTLKISRVAEDVGVYCMQGLQTPTFGGQTKLEIK 112

RESULT 8  
 ID KV2G\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01631;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (26-10).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN-A/J;  
 RX MEDLINE; 83178921.  
 RA NOVOTNY J., MARGOLIES M.N.;  
 RL BIOCHEMISTRY 22:1153-1158(1983).  
 CC -1- THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT  
 CC BINDS DIGOXIN.  
 DR PIR; A01914; KVM526.  
 DR HSP; P01607; IIGI.  
 KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.  
 FT DOMAIN 1 23 FRAMEWORK 1.



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FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; 58372CBE CRC32;

Query Match 70.1%; Score 568; DB 1; Length 113;
Best Local Similarity 76.8%; Pred. No. 8.36e-106;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Db 1 DVMTQTPLSPVSLGDAQISCRSSQLVHSGNNTYLNWYKAGQSPKLLIYKVSNR 60
QY 1 DVMTQSPSLVLTGQPASISCRSSQLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60
Db 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCAHLELPYTFGGGKLEIK 112
QY 61 SGVDPFRSGSGGDTFTLKISGVEAEDGVVYCMQFTHYPYTFGGGKLEIK 112

RESULT 9
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (REL. 02, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (17S29.1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 85128968.
RA AEBERSOLD R., HERBST H., GRUTTER T., CHANG J.Y., BRAUN D.G.;
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 365:1375-1383(1984).
CC -I- ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR: A01912; KVM517.
HSP: P01679; ICBV.
KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 6A4552AE CRC32;

Query Match 68.9%; Score 558; DB 1; Length 113;
Best Local Similarity 73.2%; Pred. No. 2.06e-103;
Matches 82; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Db 1 DVMTQAVFNPVLTGTSASISCRSSKLSHSGNTYLYWYKQKQSPQLLIYQMSNLA 60
QY 1 DVMTQSPSLVLTGQPASISCRSSQLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60
Db 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCAHLELPYTFGGGKLEIK 112
QY 61 SGVDPFRSGSGGDTFTLKISGVEAEDGVVYCMQFTHYPYTFGGGKLEIK 112

RESULT 10
ID KV2D_MOUSE STANDARD; PRT; 112 AA.
AC P01629;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

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DE IG KAPPA CHAIN V-II REGION (2S1.3).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 83055101.
RA HERBST H., CHANG J.Y., AEBERSOLD R., BRAUN D.G.;
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 363:1069-1076(1982).
CC -I- THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY
    AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01911; KVM5S1.
HSP: P01607; 4FAB.
KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; C16DB265 CRC32;

Query Match 68.1%; Score 552; DB 1; Length 112;
Best Local Similarity 72.3%; Pred. No. 5.60e-102;
Matches 81; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Db 1 DVMTQAAFSNPVLTGTSASISCRSSKLSQKSGTYLYWYKQKQSPQLLIYQMSNLA 60
QY 1 DVMTQSPSLVLTGQPASISCRSSQLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60
Db 61 SGVDPFRSGSGGDTFTLKISRVEAEDGVVYCAHLELPYTFGGGKLEIK 112
QY 61 SGVDPFRSGSGGDTFTLKISGVEAEDGVVYCMQFTHYPYTFGGGKLEIK 112

RESULT 11
ID KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-IV REGION (LEN).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 76004342.
RA SCHNEIDER M., HILSCHMANN N.;
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA SALOMON A.;
RL SUBMITTED (AUG-1996) TO THE SWISS-PROT DATA BANK.
CC -I- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01903; K4HULN.
HSP: P01607; 1MCP.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 41 55 FRAMEWORK 2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 63 94 FRAMEWORK 3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 113 FRAMEWORK 4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; EEICE0BE CRC32;

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Query Match 66.8%; Score 541; DB 1; Length 114;  
 Best Local Similarity 67.3%; Pred. No. 2,37e-99;  
 Matches 76; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

Db 1 DIVMTPSPDLAVSLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLLIYWASTR 60  
 Y 1 DIVMTPSPDLAVSLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLLIYWASTR 60  
 Db 61 EGVDPFRSGSGSDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 113  
 Y 60 EGVDPFRSGSGSDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112

RESULT 12  
 ID KV4C\_HUMAN STANDARD; PRT; 134 AA.  
 AC P06314;  
 DT 01-JAN-1988 (REL. 06, CREATED)  
 DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN PRECURSOR V-IV REGION (B17).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86041854.  
 RA MARSH P., MILLS F., GOULD H.;  
 RL NUCLEIC ACIDS RES. 13:6531-6544 (1985).  
 RN [2]  
 RP REVISION TO 76.  
 RA MARSH P.;  
 RL SUBMITTED (OCT-1986) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; X02990; G37910;  
 DR PIR; A01905; K4HUI7.  
 DR HSP; P01607; 21MN.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 20  
 FT CHAIN 21 134 IG KAPPA CHAIN V-III REGION (B17).  
 FT DOMAIN 21 43 FRAMEWORK 1.  
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 61 75 FRAMEWORK 2.  
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 83 114 FRAMEWORK 3.  
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 122 133 FRAMEWORK 4.  
 FT DISULFID 43 114 BY SIMILARITY.  
 FT NON\_TER 134 134  
 SQ SEQUENCE 134 AA; 14966 MW; BB63E06A CRC32;

Query Match 65.9%; Score 534; DB 1; Length 134;  
 Best Local Similarity 67.3%; Pred. No. 1.10e-97;  
 Matches 76; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

Db 21 DIVMTPSPDLAVSLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLLIYWASTR 80  
 Y 1 DIVMTPSPDLAVSLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLLIYWASTR 80  
 Db 81 EGVDPFRSGSGSDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 133  
 Y 60 EGVDPFRSGSGSDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112

RESULT 13  
 ID KV2A\_MOUSE STANDARD; PRT; 112 AA.  
 AC P01626;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (MOPC 167).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE; 79000273.  
 RL RUDIKOFF S., POTTER M.;  
 RL BIOCHEMISTRY 17:2703-2707 (1978).  
 CC -/- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS  
 CC PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY  
 CC CHAIN HAS ALSO BEEN DETERMINED.  
 DR PIR; A01908; KVM516.  
 DR HSP; P01679; 1CBV.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 40 54 FRAMEWORK 2.  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 62 93 FRAMEWORK 3.  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 103 112 FRAMEWORK 4.  
 FT DISULFID 23 93 BY SIMILARITY.  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 12349 MW; 84A526D0 CRC32;

Query Match 63.5%; Score 514; DB 1; Length 112;  
 Best Local Similarity 68.8%; Pred. No. 6.32e-93;  
 Matches 77; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

Db 1 DIVITQDELSPVTSGESVISCSSKSLYKDGKTYLNNWFLQRPQSPQLLYLMSTRA 60  
 Y 1 DIVMTPSPDLAVSLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLLIYWASTR 60  
 Db 61 SGVDRFSGSGSDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112  
 Y 61 SGVDRFSGSGSDTFTLTKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112

RESULT 14  
 ID KV2C\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01628;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (MOPC 511).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 81052016.  
 RA APPELLA E.;  
 RL MOL. IMMUNOL. 17:711-718 (1980).  
 CC -/- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS  
 CC PHOSPHORYLCHOLINE.  
 DR PIR; A01910; KVM51.  
 DR HSP; P01679; 1CBV.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 40 54 FRAMEWORK 2.  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 62 93 FRAMEWORK 3.  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 103 112 FRAMEWORK 4.  
 FT DISULFID 23 93 BY SIMILARITY.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12496 MW; 7926A2F7 CRC32;

Query Match 63.2%; Score 512; DB 1; Length 113;  
 Best Local Similarity 67.9%; Pred. No. 1.89e-92;  
 Matches 76; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

Db 1 DIVITQDELSPVTSGESVISCSSKSLYKDGKTYLNNWFLQRPQSPQLLYLMSTRA 60  
 Y 1 DIVMTPSPDLAVSLGERATINCKSSQSLYSNKNYLAWYQKFGQPPKLLIYWASTR 60

Db 61 SGVSDRFSGSGTDFTLTKISGVEADGVVYCOQLVEYPLTFGAGTKLEIK 112  
QY 61 SGVPDRFSGSGTDFTLTKISGVEADGVVYCMQFTHYPYTFGGTKLEIK 112

RESULT 15  
ID KV3J\_MOUSE STANDARD; PRT; 111 AA.  
AC P01662;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE (ABPC 22).  
RX MEDLINE; 79012520.  
RA MCKEAN D.J., BELL M., POTTER M.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).  
RN [2]  
RP SEQUENCE (PC 9245).  
RX MEDLINE; 79073152.  
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;  
RL NATURE 276:785-790(1978).  
CC -1- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.  
DR PIR; A01935; KVM5M6.  
DR HSSP; P01679; IACY.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12041 MW; 711C554A CRC32;

Query Match 63.0%; Score 510; DB 1; Length 111;  
Best Local Similarity 63.4%; Pred. No. 5,63e-92;  
Matches 71; Conservative 18; Mismatches 22; Indels 1; Gaps 1;

Db 1 NVLTQSPASVSLVSGRATISCRASEV-DSYGNFPMHWYQKPGQPPKLLIYASNLE 59  
QY 1 DVYMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60  
Db 60 SGVPAREFSGSGTDFTLTIDPVEADDAATYCCQNNEDPYTFGGTKLEIK 111  
QY 61 SGVPDRFSGSGTDFTLTKISGVEADGVVYCMQFTHYPYTFGGTKLEIK 112

Search completed: Thu Jan 14 17:10:43 1999  
Job time : 9 secs.

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W P S R L H  
(TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:11:00 1999; MasPar time 11.72 Seconds  
Tabular output not generated. ....475.849 Million cell updates/sec

Title: >US-08-477-989B-88  
Description: (1-112) from US08477989B.pap  
Perfect Score: 810  
Sequence: 1 DVVMTQSPSPSLVLTIGQPAS.....CMQFTHYPYFGQGTGLEIK 112

Scoring table: PAM 150  
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sprenbl6

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle  
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified  
13:sp-vertebrate 14:sp-virus

Statistics: Mean 40.288; Variance 68.199; scale 0.591

Pred. No. is the number of results predicted by the chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	630	77.8	114	11	ANTI-ACID PHOSPHATASE	1.23e-120
2	621	76.7	118	4	HRV FAB N6-VL (FRAGMENT)	1.80e-118
3	577	71.2	249	11	SINGLE CHAIN FV ANTIBIO	6.59e-108
4	516	63.7	119	11	IG KAPPA CHAIN PRECURS	2.32e-93
5	512	63.2	100	4	V KAPPA (FRAGMENT)	2.07e-92
6	505	62.3	119	11	IG KAPPA CHAIN (FRAGME	9.46e-91
7	502	62.0	119	11	IG KAPPA CHAIN (FRAGME	4.86e-90
8	501	61.9	133	11	CC49 FAB PRECURSOR (FR	8.39e-90
9	471	58.1	131	4	ANTI-HIV-1 GP120 V3 LO	1.03e-82
10	442	54.6	131	4	MONOCLONAL ANTIBODY KA	6.68e-76
11	428	52.8	107	11	KAPPA (FRAGMENT)	1.26e-72
12	426	52.6	108	4	ANTI-SDNA ANTIBODY LI	3.68e-72
13	422	52.1	113	4	HRV FAB N6-VL (FRAGMENT	3.16e-71
14	420	51.9	115	4	HRV FAB N27-VL (FRAGME	9.24e-71
15	419	51.7	105	4	LIGHT CHAIN FV ANTIBIO	1.58e-70
16	417	51.5	113	4	HRV FAB 026-VL (FRAGME	4.62e-70
17	417	51.5	114	4	HRV FAB N28-VL (FRAGME	4.62e-70
18	410	50.6	239	4	ANTI-MFL SCFV (FRAGMENT	1.97e-68
19	410	50.6	244	4	ANTI-HER3 SCFV (FRAGME	1.97e-68
20	407	50.2	244	4	SINGLE-CHAIN FV FRAGME	9.79e-68

21	405	50.0	107	4	Q99980	VASOACTIVE INTESTINAL	2.85e-67
22	404	49.9	134	4	O00619	REV25-2 (FRAGMENT)	4.87e-67
23	402	49.6	108	11	O61219	ANTI-DNA LIGHT CHAIN (	1.42e-66
24	397	49.0	116	4	O15982	RHEUMATOID FACTOR C6 L	2.05e-65
25	395	48.8	113	4	O14540	HRV FAB 027-VL (FRAGME	5.95e-65
26	391	48.3	240	4	O00289	SINGLE-CHAIN FV FRAGME	5.02e-64
27	390	48.1	99	11	P97409	TYPE II COLLAGEN ANTI-	8.55e-64
28	389	48.0	262	11	O35842	ANTI-HIV-1 REVERSE TRA	1.46e-63
29	380	46.9	118	4	O15986	RHEUMATOID FACTOR D5 L	1.74e-61
30	376	46.4	243	11	O35140	ANTI-CD30 MOAB KI-4 SC	1.46e-60
31	370	45.7	107	11	O61196	ANTI-CARCINOMA EMBRYON	3.50e-59
32	365	45.1	107	4	O99953	VASOACTIVE INTESTINAL	4.93e-58
33	359	44.3	94	4	O16079	RF-V KAPPA 1-RHEUMATOI	1.17e-56
34	356	44.0	112	4	O99822	ANTI-HIV-1 GP120 ANTIB	5.70e-56
35	354	43.7	248	11	O63818	IMMUNOTOXIN MIR-BETA 1	1.64e-55
36	351	43.3	93	4	O16078	RF-V KAPPA 1-RHEUMATOI	7.93e-55
37	344	42.5	117	4	O15358	IMMUNOGLOBULIN VARIABL	3.14e-53
38	337	41.6	127	11	O61251	ANTIGEN B-CELL RECEPT	1.23e-51
39	336	41.5	93	4	O16077	RHEUMATOID FACTOR KAPP	2.08e-51
40	334	41.2	102	11	P97408	TYPE II COLLAGEN ANTIB	5.92e-51
41	319	39.4	241	11	P97771	ANTI-CEA 79 SINGLE CHA	1.47e-47
42	296	36.5	112	4	O99516	LIGHT CHAIN FAB FRAGME	2.15e-42
43	259	32.0	81	11	O61588	G8(ANTI-MRBC HYBRIDOMA	3.25e-34
44	257	31.7	110	4	O92475	ANTI-FOLATE BINDING PR	8.89e-34
45	253	31.2	111	4	O99506	LIGHT CHAIN FAB FRAGME	6.63e-33

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	114 AA.
ID	O35971			
AC	O35971;			
DT	01-JAN-1998 (TREMBREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)			
DE	ANTI-ACID PHOSPHATASE VARIABLE LIGHT CHAIN 11 (FRAGMENT).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C;			
RA	TAKATA R., MIYAMOTO Y., HONJOH K., SOEDA T., SAKAMOTO J., MIYAMOTO T.,			
RA	HATANO S.;			
RL	SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; D50316; D1024482;			
DR	EMBL; D50138; D1024481;			
DR	PFAM; PF00047; Ig.			
FT	NON_TER 1			
FT	NON_TER 114			
SQ	SEQUENCE 114 AA; 12456 MW; 791FEA22 CRC32;			
Query Match	77.88;	Score	630;	DB 11; Length 114;
Best Local Similarity	80.48;	Pred. No.	1.23e-120;	
Matches	90;	Conservative	10;	Mismatches 12; Indels 0; Gaps 0;
Db	1	DIETQSPPLTSLVTIGQPASISCKSSQSLDSDGTYLWLLQRPQSPKRLIYLVSKLD 60		
Qy	1	DVMTQSPSPSLVLTIGQPASISCKSSQSLDSDGTYLWLLQRPQSPKRLIYLVSKLE 60		
Db	61	SGVPRFTGSGSGDTFTLKISRVEAEALGVYVCWQGTFFPOTFGGKTLEIK 112		
Qy	61	SGVPRFSGSGSGDTFTLKISGVEAEALGVYVCWQGTFFPOTFGGKTLEIK 112		
RESULT	2	PRELIMINARY;	PRT;	118 AA.
ID	O14536			
AC	O14536;			
DT	01-JAN-1998 (TREMBREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)			
DT	01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)			
DE	HRV FAB N6-VL (FRAGMENT).			
OS	HOMO SAPIENS (HUMAN).			

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-PBL;

RA ITCH K., SUZUKI T.;

RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; AB006843; D1023042; -

DR PFAM; PF00047; 19.

FT NON\_TER 118

SQ SEQUENCE 118 AA; 12804 MW; CECE507A CRC32;

Query Match 76.7%; Score 621; DB 4; Length 118;

Best Local Similarity 79.5%; Pred. No. 1.80e-118;

Matches 89; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Db 3 ELVLTQSLPSLVTPGEPASISCRSSQSLHSGNFMNDWYLQRPQSPOLLILYLSKLE 62

QY 1 DVVMTQSPSLVTLTGQPASISCRSSQSLHSGNTYLNWLLQRPQSPOLLILYLSKLE 60

Db 63 SGVPRFSGSGGTDTLTKISRVEAEDGVVYCMQGLQTPYTFGGTKLEIK 114

QY 61 SGVPRFSGSGGTDTLTKISGVEAEDGVVYCMQFTHYPTFGGTKLEIK 112

RESULT 3

ID P97512

AC P97512;

DT 01-MAY-1997 (TREMREL. 03, CREATED)

DT 01-MAY-1997 (TREMREL. 03, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMREL. 06, LAST SEQUENCE UPDATE)

DE SINGLE CHAIN FV ANTIBODY (FRAGMENT).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

[1]

RP SEQUENCE FROM N.A.

RA ARTSAENKO O., WEILER E.W., MUENTZ K., CONRAD U.;

RL J. PLANT PHYSIOL. 144:427-429(1994).

[2]

RP SEQUENCE FROM N.A.

EX MEDLINE; 96086099.

RA ARTSAENKO O., PEISKER M., ZUR NIEDEN U., FIEDLER U., WEILER E.W.,

RA MUENTZ K., CONRAD U.;

RL PLANT J. 8:745-750(1995).

DR EMBL; Z29480; E283450; -

DR PFAM; PF00047; 19.

FT NON\_TER 1

SQ SEQUENCE 249 AA; 26839 MW; 428B904E CRC32;

Query Match 71.2%; Score 577; DB 11; Length 249;

Best Local Similarity 71.4%; Pred. No. 6.59e-108;

Matches 80; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

Db 135 DIETQSPSVVIVPGESVISCRSKSLLYSDGSYLFWFQRPQSPOLLIRYMSNLA 194

QY 1 DVVMTQSPSLVTLTGQPASISCRSSQSLHSGNTYLNWLLQRPQSPOLLILYLSKLE 60

Db 195 SGVPRFSGSGGTDTLTKISRVEAEDGVVYCMQHREYPLTFGAGTKLEK 246

QY 61 SGVPRFSGSGGTDTLTKISGVEAEDGVVYCMQFTHYPTFGGTKLEIK 112

RESULT 4

ID O55115

AC O55115;

DT 01-JUN-1998 (TREMREL. 06, CREATED)

DT 01-JUN-1998 (TREMREL. 06, LAST SEQUENCE UPDATE)

DE IG KAPPA CHAIN PRECURSOR (FRAGMENT).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

[1]

RP SEQUENCE FROM N.A.

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-LIVER;

RX MEDLINE; 87110625.

RA CORBET S., MILILI M., FOUGEREAU M., SCHIFF C.;

RL J. IMMUNOL. 138:932-939(1987).

DR EMBL; D00080; D1000493; -

KW SIGNAL.

FT SIGNAL 1

FT CHAIN 20

FT NON\_TER 119

SQ SEQUENCE 119 AA; 13079 MW; 6B5A6578 CRC32;

Query Match 63.7%; Score 516; DB 11; Length 119;

Best Local Similarity 77.0%; Pred. No. 2.32e-93;

Matches 77; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Db 20 DVVMTQTPSLVTPGEPASISCRSSQSLVHSGNTYLNWLLQRPQSPOLLILYLSKLE 79

QY 1 DVVMTQSPSLVTLTGQPASISCRSSQSLHSGNTYLNWLLQRPQSPOLLILYLSKLE 60

Db 80 SGVPRFSGSGGTDTLTKISRVEAEDGVVYCMQSTHYP 119

QY 61 SGVPRFSGSGGTDTLTKISGVEAEDGVVYCMQFTHYP 100

RESULT 5

ID Q15535

AC Q15535;

DT 01-NOV-1996 (TREMREL. 01, CREATED)

DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)

DT 01-AUG-1998 (TREMREL. 07, LAST SEQUENCE UPDATE)

DE V KAPPA (FRAGMENT).

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

[1]

RP SEQUENCE FROM N.A.

RA KATO S., TACHIBANA K., TAKAYAMA N., KATAOKA H., YOSHIDA M.C.,

RA TAKANO T.;

RL SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; D90161; G1262585; -

DR PFAM; PF00047; 19.

FT NON\_TER 1

SQ SEQUENCE 100 AA; 10871 MW; 06A1440D CRC32;

Query Match 63.2%; Score 512; DB 4; Length 100;

Best Local Similarity 79.0%; Pred. No. 2.07e-92;

Matches 79; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Db 1 DVVMTQTPSLVTPGEPASISCRSSQSLHSGNTYLNWLLQRPQSPOLLILYLSKLE 60

QY 1 DVVMTQSPSLVTLTGQPASISCRSSQSLHSGNTYLNWLLQRPQSPOLLILYLSKLE 60

Db 61 SGVPRFSGSGGTDTLTKISRVEAEDGVVYCMQIHLP 100

QY 61 SGVPRFSGSGGTDTLTKISGVEAEDGVVYCMQFTHYP 100

RESULT 6

ID O55116

AC O55116;

DT 01-JUN-1998 (TREMREL. 06, CREATED)

DT 01-JUN-1998 (TREMREL. 06, LAST SEQUENCE UPDATE)

DE IG KAPPA CHAIN (FRAGMENT).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

[1]

RP SEQUENCE FROM N.A.

```

RC STRAIN-BALB/C; TISSUE=LIVER;
RX MEDLINE: 87110625;
RA CORBET S.; MILLI M., FOUGEREAU M., SCHIFF C.;
RL J. IMMUNOL. 138:932-939(1987).
DR EMBL; D00081; D1000494; -
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13117 MW; C201F8D8 CRC32;

Query Match 62.38; Score 505; DB 11; Length 119;
Best Local Similarity 75.08; Pred. No. 9.46e-91;
Matches 75; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Db 20 DVLMTOTELSLPVSLGDOASISCRSSOSIVHSNGTNTVLEWYLOKPGSPQLLIYVSNRF 79
QY 1 DVVMTQSPPSLLVTLGQPASISCRSSOSLLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 80 SGVDFRFGSGSGTDFTLKISGVEAEDLVGYCYFQGSHPV 119
QY 61 SGVDFRFGSGSGTDFTLKISGVEAEDVGYYCMQFTHYP 100

RESULT 7
ID Q05117 PRELIMINARY; PRT; 119 AA.
AC Q05117
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=LIVER;
RX MEDLINE: 87110625
RA CORBET S.; MILLI M., FOUGEREAU M., SCHIFF C.;
RL J. IMMUNOL. 138:932-939(1987).
DR EMBL; D00082; D1000495; -
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13117 MW; 7D3761A1 CRC32;

Query Match 62.08; Score 502; DB 11; Length 119;
Best Local Similarity 76.08; Pred. No. 4.86e-90;
Matches 76; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Db 20 DAYMTOTELSLPVSLGDOASISCRSSOSLNSGNTYLNWYLOKPGSPQLLIYVSNRF 79
QY 1 DVVMTQSPPSLLVTLGQPASISCRSSOSLLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60

Db 80 SGVDFRFGSGSGTDFTLKISGVEAEDLVGYFCLQVTHVP 119
QY 61 SGVDFRFGSGSGTDFTLKISGVEAEDVGYYCMQFTHYP 100

RESULT 8
ID Q61551 PRELIMINARY; PRT; 133 AA.
AC Q61551
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE CC49 FAB PRECURSOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA ABERGEL C.; PADLAN E.A., KASHMIRI S.V.S., MILENIC D., CALVO B.,
RA SCHLOM J.;
RL SUBMITTED (JUN-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; M95574; G193215; -
KW SIGNAL.
FT NON_TER 1 20 POTENTIAL.

RC STRAIN-BALB/C; TISSUE=LIVER;
RX MEDLINE: 87110625;
RA CORBET S.; MILLI M., FOUGEREAU M., SCHIFF C.;
RL J. IMMUNOL. 138:932-939(1987).
DR EMBL; D00081; D1000494; -
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13117 MW; C201F8D8 CRC32;

Query Match 61.9%; Score 501; DB 11; Length 133;
Best Local Similarity 61.9%; Pred. No. 8.39e-90;
Matches 70; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

Db 21 DIVMSQSPSSLPVSGEKVTLSCSKSSQSLYSGNKNYLAWYQKPGSPQLLIYVASAR 80
QY 1 DVVMTQSPPSLLVTLGQPASISCRSSOSLLHSSG-NTYLNWLLQRPQSPQPLIYLVSKL 59

Db 81 ESGVDPDRFGSGSGTDFTLSSIVSKTDLAVYCYQYISYPLTFCAGTKVLK 133
QY 60 ESGVDPDRFGSGSGTDFTLKISGVEAEDVGYYCMQFTHYPYTFGQGTGLEIK 112

RESULT 9
ID Q99826 PRELIMINARY; PRT; 115 AA.
AC Q99826
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ANTI-HIV-1 GP120 V3 LOOP ANTIBODY D0142-10 LIGHT CHAIN VARIABLE REGION
(FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA DITZEL H.J., PARREN P.W.H.I., BINLEY J.M., SODROSKI J., MOORE J.P.,
RA BARBAS C.F., BURTON D.R.;
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U82962; G1800287; -
DR PFAM; PF00047; 1g.
FT NON_TER 1 115
SQ SEQUENCE 115 AA; 12740 MW; 745D103A CRC32;

Query Match 58.18; Score 471; DB 4; Length 115;
Best Local Similarity 60.0%; Pred. No. 1.03e-82;
Matches 66; Conservative 23; Mismatches 20; Indels 1; Gaps 1;

Db 4 LTQSPDSLAVSLGERATINCKSSOTVFVNSKNKNYLAWYQKSGPELLISWASTRESG 63
QY 4 MTQSPPELLVTLGQPASISCRSSOSLLHSSGNT-YNWLLQRPQSPQPLIYLVSKLESG 62

Db 64 VPDFRFGSGSGTDFTLTSSLAQEDVAVYCYQYINVPFTFGPGTKVDIK 113
QY 63 VPDFRFGSGSGTDFTLKISGVEAEDVGYYCMQFTHYPYTFGQGTGLEIK 112

RESULT 10
ID Q99671 PRELIMINARY; PRT; 131 AA.
AC Q99671
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE MONOCLONAL ANTIBODY KAPPA CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA RYU C.J., JIN B.R., CHUNG H.K., HONG H.J.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U66190; G1778126; -
DR PFAM; PF00047; 1g.
KW SIGNAL.
FT NON_TER 1 22 POTENTIAL.
FT CHAIN 23 >131 MONOCLONAL ANTIBODY KAPPA CHAIN VARIABLE
FT NON_TER 131 131 REGION.

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Best Local Similarity 55.4%; Pred.No. 3,68e-72;
Matches_ 62; Conservative 26; Mismatches 19; Indels 5; Gaps 3;
```

Dbb 1 EIVMTSPATLSVSGERATLSCRASQSF--TS-K--LGWYQQKPGCAPRLLIYGASTRA 55  
::| | | | | :: : : : : : | | | : : - - - | : | | : | | |  
Qy 1 DVVMTSQPSLLVTLCQPASISCRSSQLHSSGNTYLNWLQRPGSQPPLIYLVSLE 60  
:-| | | | | ::| | | | | : : : : : | : : | : | | | : | | |

Ddb 56 TGIPARFSGSGGTFTLTATISSQSDFAVYYCQYNMPLTFGGQTKEIK 107  
:-| | | | | ::| | | | | : : : : : | : : | : | | | : | | |  
Qy 61 SGVPDRFGSGSGTDTFLTKISGVEADVGYICMQTHYPYTFGGTKLEIK 112  
:-| | | | | ::| | | | | : : : : : | : : | : | | | : | | |

RESULT 13  
ID O14535 PRELIMINARY; PRT; 113 AA.  
AC O14535;  
DT 01-JAN-1998 (TREMBREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)  
DE HRV FAB N6-VL (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PBL;  
RA ITOH K., SUZUKI T.;  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.  
DR.. EMBL.: AB006842; D1023041; -.  
DR PFAM: PF00047; Ig. 113  
FT NON\_TER 113  
SQ SEQUENCE 113 AA; 12207 MW; A546C704 CRC32;

Query Match 52.1%; Score 422; DB 4; Length 113;  
Best Local Similarity 58.0%; Pred.No. 3,16e-71;  
Matches 65; Conservative 20; Mismatches 22; Indels 5; Gaps 2;

Ddb 3 ELVMTQSPSLAAVGSDRVFTFCRASQSI--SS---YLNWYQQKPKAPKLIIYAASSLQ 57  
:| | | | | : : : : : | | | | | : : : : : | | | : | | |  
Qy 1 DVVMTSQPSLLVTLCQPASISCRSSQLHSSGNTYLNWLQRPGSQPPLIYLVSLE 60  
:-| | | | | ::| | | | | : : : : : | : : | : | | | : | | |

Ddb 58 SGVPDRFGSGSGTDTFLTATISSLOPEDFYATYCQSYSTPIFFGQTRLEIK 109  
|| || || || || || || || || || : : : : : | | | | | : | | | | |  
Qy 61 SGVPDRFGSGSGTDTFLTKISGVEADVGYICMQTHYPYTFGGTKLEIK 112  
:-| | | | | ::| | | | | : : : : : | : : | : | | | : | | |

RESULT 14  
ID O14537 PRELIMINARY; PRT; 115 AA.  
AC O14537;  
DT 01-JAN-1998 (TREMBREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)  
DE HRV FAB N27-VL (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PBL;  
RA ITOH K., SUZUKI T.;  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.  
DR EMBL: AB006844; D1023043; -.  
DR PFAM: PF00047; Ig. 115  
FT NON\_TER 115  
SQ SEQUENCE 115 AA; 12417 MW; 96E3C279 CRC32;

Query Match 51.9%; Score 420; DB 4; Length 115;  
Best Local Similarity 57.5%; Pred.No. 9,24e-71;  
Matches 65; Conservative 21; Mismatches 22; Indels 5; Gaps 3;

Ddb ... 3 ELTLTQSPGLTSLSPGERATLSCRASQSV--SS--SYLAWYQQKPGCAPRLLIYGASSRA 58  
: : | | | : : : : | | | | | : : | | | : : | | | : | | | : | | |  
Qy 1 DVVMTSQPSLLVTLCQPASISCRSSQLHSSGNTYLNWLQRPGSQPPLIYLVSLE 60  
:-| | | | | ::| | | | | : : : : : | : : | : | | | : | | |

Search completed: Thu Jan 14 17:11:35 1999  
Job time : 35 secs.



(TM)

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Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	724	89.4	253	11	R59083	Protein encoded from	5.86e-48
2	712	87.9	134	11	R59078	LO-CD2a VL and signal	5.49e-47
3	638	78.8	272	29	W43913	Mus musculus antibody	5.20e-41
4	631	77.9	272	18	W00557	Nematode salivary pro	1.91e-40
5	627	77.4	135	24	W24989	Monoclonal antibody 2	4.00e-40
6	627	77.4	135	10	R34052	Sequence of the VL re	4.00e-40
7	627	77.4	135	20	W01535	Monoclonal antibody 2	4.00e-40
8	627	77.4	535	24	W28492	Human p53 protein var	4.00e-40
9	627	77.4	535	24	W28491	Human p53 protein var	4.00e-40
10	623	76.9	112	5	R24710	Sequence of a chimeri	8.40e-40
11	623	76.9	132	5	R24712	Sequence encoded by t	8.40e-40
12	620	76.8	112	19	R52057	Light chain variable	1.01e-39
13	620	76.5	112	29	W48248	A7 anti-Fc alpha R a	1.47e-39
14	618	76.3	132	2	R12361	Lght (kappa) chain v	2.14e-39
15	614	75.8	131	2	R12359	Mouse Mab 4d12 L chal	4.45e-39
16	609	75.2	113	29	W39897	Light chain of the ca	1.12e-38
17	608	75.1	141	6	R30454	C342:11 MAB kappa cha	1.35e-38
18	608	75.1	141	6	R32541	C242 kappa chain vari	1.35e-38

119	605	74.7	133	7	R33951	CTM01.VL.	2.36e-33
120	601	74.2	112	29	W40133	Human Mab AB17.1.41 p	4.95e-38
121	601	74.2	112	19	R95212	HumB3V1 humanised var	4.95e-38
122	598	73.8	114	29	R39805	Variable domain of th	8.62e-38
123	597	73.7	113	1	R56652	Anti-CMV monoclonal a	1.04e-37
124	596	73.6	110	7	R38159	Sequence of the light	1.25e-37
125	595	73.5	112	19	R95218	Human IgM GM607 varia	1.50e-37
126	594	73.3	263	3	R15055	Qm212 single chain an	1.81e-37
127	593	73.2	112	6	R32329	Humanised Mab light c	2.17e-37
128	593	73.2	112	26	W27145	Mature light chain va	2.17e-37
129	593	73.2	238	17	R93554	Monoclonal antibody D	2.17e-37
130	592	73.1	131	10	R53822	Humanised murine KC-4	2.62e-37
131	592	73.1	131	13	R70470	Humanised anti-KC-4 a	2.62e-37
132	591	73.0	113	17	R85808	Vlkappa for antibody	3.15e-37
133	590	72.8	253	16	R72599	Anti-daunsyl single ch	3.79e-37
134	589	72.7	239	13	R65757	Anti-tobacco mosaic v	4.56e-37
135	588	72.6	238	22	W14937	Murine anti-porcine v	5.48e-37
136	588	72.6	238	22	W14942	3F4 Human IgG4 expres	5.48e-37
137	586	72.3	114	25	W27544	Human Ab light chain	7.94e-37
138	586	72.3	239	5	R24811	Sequence encoded by t	7.94e-37
139	586	72.3	281	25	W27560	Consensus single chai	7.94e-37
140	585	72.2	112	3	R14393	Modified L3 region of	9.55e-37
141	583	72.0	112	3	R14392	L3 region of kappa l1	1.38e-36
142	581	71.7	238	10	R58664	4-4-20.VL / 217 / CC4	2.00e-36
143	580	71.6	133	25	W29751	Anti-HMG Mab CTM01	2.41e-36
144	578	71.4	149	20	W03199	Anti-Idiotypic monoclo	3.48e-36
145	576	71.1	241	7	R37645	Sequence of a multia	5.04e-36

cc represents the coding region for the LO-CD2a Tg/nc chain variant.

CC from the antibody LO-CD2a, and the leader sequence from the LOCD2a gene.  
 CC LO-CD2a is produced by the cell line ATCC HB 11423. It is pref. a rat  
 CC monoclonal antibody and is produced using CD2. This antibody, or  
 CC fragments of it, binds to all T lymphocytes and also to null cells but  
 CC not to B lymphocytes. It binds to all CD4 and CD8 positive cells as  
 CC defined by Leu3a and Leu2b antibodies respectively. LO-CD2a can be used  
 CC for inhibiting an immune response in a human patient, partic. an immune  
 CC response mediated by T cell activation and proliferation resulting from  
 CC graft transplantation, graft-versus-host disease or autoimmune diseases.  
 CC The missing residues are deduced from the DNA sequence given in the  
 CC specification.  
 SQ Sequence 253 AA;

Query Match 89.4%; Score 724; DB 11; Length 253;  
 Best Local Similarity 87.5%; Pred. No. 5.86e-48;  
 Matches 98; Conservative 9; Mismatches 5; Indels 0; Gaps 0;  
 Db 142 dvltqtptllatigqsvsicsrssqslhssgntynllwllqrgqspqpllylvskle 201  
 QY 1 DVMTQSPSPSLVLTGQPASISCRSSQSLHSSGNTYNLLWLLQRPQSPQPLIYLVSKLE 60  
 Db 202 sgvpnhfsgsgtdftlkisgveaedlgvvyqcmfthpytfgagtklelk 253  
 QY 61 SGVPDRFSGSGTDTFTLKISGVEAEDGVVYCMQFTHPYTFTFGGQTKLEIK 112

RESULT 2  
 ID R59078 standard; Protein; 134 AA.  
 AC R59078;

DE 27-APR-1995 (first entry)  
 DE LO-CD2a VL and signal peptide from MRC vector hcmv-vlyls-kr-neo.  
 KW signal sequence; MRC; vector; hcmv-vlyls-kr-neo; ATCC HB 11423;  
 KW monoclonal antibody; MAb; T lymphocyte; null cell; B lymphocyte;  
 KW CD4; CD8; Leu3a; Leu2b; inhibition; immune response; human;  
 KW T cell; activation; proliferation; graft transplantation;  
 KW graft-versus-host disease; autoimmune disease.  
 OS Rattus rattus.

FH Key Location/Qualifiers  
 FT peptide 1..22 /note= "Signal peptide"  
 FT protein 23..134 /note= "LO-CD2a VL"  
 FT misc\_difference 13 /note= "Encoded by CTT"  
 FT misc\_difference 15 /note= "Encoded by TTT"  
 FT misc\_difference 93..94 /note= "Encoded by CGGTCA"  
 FT misc\_difference 103 /note= "Encoded by AGT"  
 FT misc\_difference 105 /note= "Encoded by CTG"  
 FT misc\_difference 112 /note= "Encoded by CTT"  
 FT misc\_difference 128 /note= "Encoded by GGG"

PN W09420619-A.  
 PD 15-SEP-1994.  
 PF 04-MAR-1994; IB0043.  
 PR 05-MAR-1993; US-027008.  
 PR 09-SEP-1993; US-119032.  
 PA (UVLO-) UNIV CATHOLIQUE LOUVAIN.  
 PI Bazin H, Latinne D;  
 PI WPI; 94-303026/37.  
 DR N-PSDB; Q71875.  
 DR New anti-CD2 monoclonal antibody - used for inhibiting an immune  
 PT response mediated by T cell activation and proliferation  
 PS Claim 29; Fig 29A; 101pp; English.  
 CC This sequence represents the LO-CD2a light chain variable region from  
 CC the antibody LO-CD2a, and the signal sequence from the MRC vector hcmv-  
 CC vlyls-kr-neo. LO-CD2a is produced by the cell line ATCC HB 11423; it  
 CC is pref. a rat monoclonal antibody and is produced using CD2. This

CC antibody, or fragments of it, binds to all T lymphocytes and also to  
 CC null cells but not to B lymphocytes. It binds to all CD4 and CD8.  
 CC positive cells as defined by Leu3a and Leu2b antibodies respectively.  
 CC LO-CD2a can be used for inhibiting an immune response in a human  
 CC patient, partic. an immune response mediated by T cell activation  
 CC and proliferation resulting from graft transplantation, graft-versus-  
 CC host disease or autoimmune diseases.  
 SQ Sequence 134 AA;

Query Match 87.9%; Score 712; DB 11; Length 134;  
 Best Local Similarity 85.7%; Pred. No. 5.49e-47;  
 Matches 96; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 23 dqltqspptllatigqsvsicsrssqslhssgntynllwllqrgqspqpllylvskle 82  
 QY 1 DVMTQSPSPSLVLTGQPASISCRSSQSLHSSGNTYNLLWLLQRPQSPQPLIYLVSKLE 60  
 Db 83 sgvpnhfsgsgtdftlkisgveaedlgvvyqcmfthpytfgagtklelk 134  
 QY 61 SGVPDRFSGSGTDTFTLKISGVEAEDGVVYCMQFTHPYTFTFGGQTKLEIK 112

RESULT 3  
 ID W43913 standard; Protein; 272 AA.  
 AC W43913;

DE 17-JUN-1998 (first entry)  
 DE Mus musculus antibody specific for cyst nematode salivary protein.  
 KW Cellulase activity; nematode; crop protection; parasitic;  
 KW subventral oesophageal protein; cyst nematode;  
 KW salivary protein.  
 OS Mus musculus.

FH Key Location/Qualifiers  
 FT Domain 1..112 /note= "antibody variable domain light chain"  
 FT Region 25..39 /note= "Complementarity Determining Region"  
 FT Region 55..61 /note= "Complementarity Determining Region"  
 FT Region 93..102 /note= "Complementarity Determining Region"  
 FT Peptide 113..127 /note= "Gly-Ser peptide linker"  
 FT Domain 128..273 /note= "antibody variable domain heavy chain"  
 FT Region 158..162 /note= "Complementarity Determining Region"  
 FT Region 529..579 /note= "Complementarity Determining Region"  
 FT Region 226..232 /note= "Complementarity Determining Region"  
 FT Region /note= "Complementarity Determining Region"

PN EP-818538-A1.  
 PD 14-JAN-1998.  
 PF 08-JUL-1996; 201890.  
 PR 08-JUL-1996; EP-201890.  
 PA (RIJK-) RIJSLANDBOUWUNIVERSITEIT WAGENINGEN.  
 PI Bakker J, De Boer JM, Gommers EJ, Govers A, Helder J,  
 PI Roosen J, Schots A, Schouten A, Smant G, Stiekema WJ,  
 PI Stokkermans JFW;  
 PI WPI; 98-065307/07.  
 DR N-PSDB; T86646.  
 DR Nematodal cellulase peptide(s) - useful as industrial cellulolytic  
 PT enzymes or for plant protection  
 PS Example; Pages 22-24; 28pp; English.  
 CC The sequence is that encoding a peptide fragment of an antibody  
 CC specific for a salivary protein of cyst nematodes. It can be used  
 CC to help protect plants against parasitic nematodes.  
 SQ Sequence 272 AA;

Query Match 78.8%; Score 638; DB 29; Length 272;  
 Best Local Similarity 81.3%; Pred. No. 5.20e-41;  
 Matches 91; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Db 1 dvmtqtptllatigqsvsicsrssqslhssgntynllwllqrgqspqpllylvskle 60



<p>Monoclonal antibody; diagnosis; treatment; infection; hepatitis B; xenogeneic hybridoma; SPAZ 4; PEI-1; ZMI-1; ZMI-2; MD3-4; L03-3; IgG1 class; heavy chain; light chain; variable region. Homo sapiens.</p>					
Key	Location/Qualifiers				
peptide	1..22				
/label= leader_sequence					
region	23..122				
/label= V_kappa_III_region					
region	23..45				
/label= framework_region					
region	46..62				
/label= CDR1					
region	63..76				
/label= framework_region					
region	77..83				
/label= CDR2					
region	84..115				
/label= Framework_region					
region	116..124				
/label= CDR3					
region	123..135				
/label= J_kappa_5 region					
US556354-A.					
IPN	PD	15-OCT-1996.			
DDR	PPF	05-SEP-1986;	904517.		
PPT	PPR	05-SEP-1986;	US-904517.		
PPT	PPR	31-OCT-1986;	US-925196.		
PPS	PPR	11-MAY-1988;	US-192754.		
CCC	PPR	15-JUN-1988;	US-538796.		
CCC	PPR	27-MAR-1991;	US-676036.		
CCC	PPR	21-APR-1992;	US-871426.		
CCC	PPR	14-JUN-1994;	US-259372.		
CCC	PPA	(SANO ) SANDOZ LTD.			
PPI	DRD	Ostberg IG;	96-476304/47.		
DDR	DRD	N-PSDB; T46131.			
PPT	PPT	Human monoclonal antibodies specific for hepatitis B surface antigen			
PPT	PPT	- are used to treat or prevent infection or in diagnostic assays			
PPS	PPS	Example 9; Column 39-40; 26pp; English.			
CCC	CCC	Monoclonal antibodies effective for the diagnosis and treatment of			
CCC	CCC	diseases caused by infection with hepatitis B have been prepared from a			
CCC	CCC	cell line obtained by fusing a xenogeneic hybridoma designated SPAZ 4			
CCC	CCC	with blood cells of a patient immunised with hepatitis B vaccine.			
CCC	CCC	Specific antibodies are PEI-1, ZMI-1, ZMI-2, MD3-4 and L03-3, each of			
CCC	CCC	these being of the IgG1 class. The present sequence is the light			
CCC	CCC	variable chain of ZMI-1.			
SQ		Sequence 135 AA;			
Query Match	77.4%;	Score 627;	DB 20;	Length 135;	
Best Local Similarity	82.1%;	Pred. No. 4.00e-40;			
Matches	92;	Conservative	7;	Mismatches 13;	Indels 0; Gaps 0;
Ddb	23	dvvvtqslsplvptlgqpasiscrsalsldvsdgtynlwnflgrpgsqprlllyqlssrd	82		
QY	1	DVVMQTSPPELVLTGQPASISCRSSQSLLHSSGNTYLWLLQLRPQSQPOLLYLVSLE 60			
Ddb	83	sypvdrfsgsgsgtaftklisrveaedgvyyvcmgcthwplifgggtrleik	134		
QY	61	SGVPDRFGSGSGTDTTLKISGVEADGVYYCMQTHYPYTFGGGTKEIK	112		
RESULT 8					
IID	W28492	standard; Protein; 535 AA.			
AC	W28492;				
DE	25-NOV-1997	(first entry)			
KDE	Human p53 protein variant S-325H.				
KKW	Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;				
KKW	substitution; replacement; transactivation; viral protein VP16; HSV;				
KKW	anti-oncogene; hyperproliferation; cancer; restenosis; SCFv;				
KKW	tumour suppression; apoptosis; single chain antibody variable domain.				
OS	Chimeric - Homo sapiens.				
OS	Chimeric - Herpes simplex virus.				

OS Synthetic. Location/Qualifiers.  
 FH Key misc\_difference 361  
 FT /note= "Arg residue at position 182 of wild-type  
 FT p53 has been mutated to His"  
 PD WO9704092-A1.  
 PN 06-FEB-1997.  
 PR 17-JUL-1996; F01111.  
 PR 19-JUL-1995; FR-008729.  
 PA (RHON ) RHONE POULENC RORER SA.  
 PI Bracco L, Conseiller E;  
 DR WPI: 97-132633/12.  
 PT New p53 variants e.g. with oligomerisation domain replaced by  
 PT leucine zipper - useful for treating hyper-proliferative disorders,  
 PT esp. cancer and restenosis  
 PS Claim 36; Page -; 133pp; French.  
 CC Claimed variants of protein p53 have at least part of the  
 CC oligomerisation domain deleted and replaced by a leucine zipper  
 CC domain. The mutants preferably also have at least part of the p53  
 CC transactivation domain (amino acids 1-74) deleted and replaced by  
 CC the transactivating domain (TD) from herpes simplex virus viral  
 CC protein VP16 (amino acids 411-490) or by a protein domain able to  
 CC bind selectively to a transactivator, especially a single-chain  
 CC antibody variably domain (ScFv). The present sequence is that of  
 CC a ScFv domain, amino acids 75-325 of human wild-type p53 and a  
 CC leucine zipper domain at the C-terminal. The p53 variants are  
 CC more active and more stable tumour suppressors and apoptosis-inducing  
 CC agents than wild-type p53 and are active where the wild-type protein  
 CC is not, i.e. they are not inactivated by dominant negative or oncogenic  
 CC mutants, nor by other cellular proteins (because the leucine zipper  
 CC domain prevents formation of inactive mixed oligomers).  
 CC Sequence 535 AA;  
 SQ  
 Query Match 77.4%; Score 627; DB 24; Length 535;  
 Best Local Similarity 79.5%; Pred. NO. 4.00e-40;  
 Matches 89; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
 Sequence 535 AA;  
 Db 134 dvlmtqptltlsvtvgpasiscsksgslldsgdgtynllwllqrggspkrllylvskld 193  
 QY 1 DVVMTQSPSPSLDLTVLQGPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60  
 Db 194 sgvdrtfgsgsgtdftlklnrveedlgvycwgthsphtfgagtklelk 245  
 QY 61 SGVPRFSGSGSDFTLKISGVEADGVYICMQFTHTPTFTFGQGTLEIK 112  
 RESULT 9  
 ID W28491 standard; Protein; 535 AA.  
 AC W28491.  
 DT 25-NOV-1997 (first entry)  
 DE Human p53 protein variant S-325 encoded by p53176.  
 KW Leucine zipper domain; L2D; oligomerisation domain; mutant; mutein;  
 KW substitution; replacement; transactivation; viral protein VP16; HSV;  
 KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;  
 KW tumour suppression; apoptosis; single chain antibody variable domain.  
 OS Chimeric - Homo sapiens.  
 OS Synthetic.  
 OS Chimeric - Herpes simplex virus.  
 PN WO9704092-A1.  
 PD 06-FEB-1997.  
 PR 17-JUL-1996; F01111.  
 PR 19-JUL-1995; FR-008729.  
 PA (RHON ) RHONE POULENC RORER SA.  
 PI Bracco L, Conseiller E;  
 DR WPI: 97-132633/12.  
 DR N-PSD: 186221.  
 PT New p53 variants e.g. with oligomerisation domain replaced by  
 PT leucine zipper - useful for treating hyper-proliferative disorders,  
 PT esp. cancer and restenosis

PS Claim 36; Pages 88-90; 133pp; French.  
 CC Claimed variants of protein p53 have at least part of the  
 CC oligomerisation domain deleted and replaced by a leucine zipper  
 CC domain. The mutants preferably also have at least part of the p53  
 CC transactivation domain (amino acids 1-74) deleted and replaced by  
 CC the transactivating domain (TD) from herpes simplex virus viral  
 CC protein VP16 (amino acids 411-490) or by a protein domain able to  
 CC bind selectively to a transactivator, especially a single-chain  
 CC antibody variably domain (ScFv). The present sequence is that of  
 CC a ScFv domain, amino acids 75-325 of human wild-type p53 and a  
 CC leucine zipper domain at the C-terminal. The p53 variants are  
 CC more active and more stable tumour suppressors and apoptosis-inducing  
 CC agents than wild-type p53 and are active where the wild-type protein  
 CC is not, i.e. they are not inactivated by dominant negative or oncogenic  
 CC mutants, nor by other cellular proteins (because the leucine zipper  
 CC domain prevents formation of inactive mixed oligomers).  
 CC Sequence 535 AA;  
 SQ  
 Query Match 77.4%; Score 627; DB 24; Length 535;  
 Best Local Similarity 79.5%; Pred. NO. 4.00e-40;  
 Matches 89; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
 Sequence 535 AA;  
 Db 134 dvlmtqptltlsvtvgpasiscsksgslldsgdgtynllwllqrggspkrllylvskld 193  
 QY 1 DVVMTQSPSPSLDLTVLQGPASISCRSSQSLHSSGNTYLNWLLQRPQSPQPLIYLVSKLE 60  
 Db 194 sgvdrtfgsgsgtdftlklnrveedlgvycwgthsphtfgagtklelk 245  
 QY 61 SGVPRFSGSGSDFTLKISGVEADGVYICMQFTHTPTFTFGQGTLEIK 112  
 RESULT 10  
 ID R24710 standard; Protein; 112 AA.  
 AC R24710.  
 DT 28-DEC-1992 (first entry)  
 DE Sequence of a chimeric anti-human fibrin antibody light chain  
 DE variable region contg. complementarity determining regions (CDRs)  
 DE A, B and C.  
 KW Chimeric monoclonal antibody; anti-fibrin antibody;  
 KW antithrombotic agent; myocardial infarction therapy.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT region /label= CDR A  
 FT region /label= CDR B  
 FT region /label= CDR C  
 PN EP-491351-A.  
 PD 24-JUN-1992.  
 PR 17-DEC-1991; 121591.  
 PR 18-DEC-1990; JP-413829.  
 PR 11-NOV-1991; JP-294464.  
 PA (TAKEDA ) TAKEDA CHEM IND LTD.  
 PI Iwasa S, Taka H, Watanabe T, Tada H;  
 DR WPI: 92-209528/26.  
 PT Chimeric monoclonal antibodies - contain anti-human fibrin  
 PT antibody light and heavy chain variable and constant for treating  
 PT thrombotic conditions e.g. myocardial infarction  
 PS Disclosure; Page 8; 87pp; English.  
 CC The inventors claim a chimeric monoclonal antibody which contains an  
 CC anti-human fibrin antibody light chain variable region contg. at  
 CC least one of the polypeptide chains A, B and C (R24704, R24705, R24706)  
 CC and a human antibody light chain constant region. A prefid. chimeric  
 CC monoclonal antibody contains all three complementarity determining  
 CC regions. The chimeric Abs can be used both in vivo and in vitro  
 CC and, since they have very low immunogenicity as compared with mouse  
 CC Abs, they can be administered to humans for diagnostic and  
 CC therapeutic purposes. They are also more stable and show a longer  
 CC half-life in the blood as compared with the original mouse Abs.  
 CC Sequence 112 AA;  
 SQ

QY 61 SGVPDRFSGSGSDFTLKISGVEADVGVYCMQFTHYPYTFGGQTKLEIK 112

RESULT	12
ID	R52057 standard; Protein; 113 AA.
AC	R52057;
DT	10-OCT-1996 (first entry)
DE	Light chain variable region of human KV2F antibody.

DE Light chain variable region of human KV2F antibody.  
KW antibody; humanised; murine; human; heavy chain; light; variable;  
KW framework region; complementarity determining region; reshaping;  
KW modelling; surface residue; modify.

OS	Homo sapiens.	Location/Qualifiers
FH	Key	

File	Key	Location/Qualifiers
FT	region	1..23
FT		/label= "framework_region_1
FT		/note= "FR 1"
FT	region	24..39
FT		/label= "complementarity_determining_region_1
FT		/note= "CDR 1"
FT	region	40..54
FT		/note= "FR 2"
FT	region	55..61
FT		/note= "CDR 2"
FT	region	62..95
FT		/note= "FR 3"
FT	region	96..105
FT		/note= "CDR 3"

FT	33..61	/note= "CDR 2"
FT	62..95	/note= "FR 3"
FT	96..105	/note= "CDR 3"
FT		
PN	EP-592106-A1.	
PD	13-APR-1994.	
PF	07-SEP-1993; 307051.	
PR	09-SEP-1992; US-942245.	
PA	(PEDE/) PEDERSEN J T.	
PA	(IMMU-) IMMUNOGEN INC.	
PI	Guilid BC, Pedersen JT,	Rees AR, Roguska MA, Searle SMJ;
PT	WPI; 94-120230/15.	
PT	Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved therapeutic efficiency by presenting human surface on V-region Example 1; Fig 4B; 230pp; English.	
PS	Modification of a rodent antibody (Ab) or fragment by resurfacing in order to produce a humanised rodent Ab can be determined by calculating homology between murine and human Ab antibody surfaces. In order to test the resurfacing approach of the invention, three humanisation experiments were set up: (1) traditional loop grafting; (2) resurfacing approach using most similar chain; and (3) resurfacing approach using human sequences with most similar surface residues. The Ab used was the murine anti-N901 Ab (see R52055). Experiment 2 was carried out using the present sequence which represents the human KV2F Ab light chain variable region with 87 percent homology with anti-N901 Ab. N901/KV2F (R52058) was prepared by CDR grafting.	
SC	Sequence 113 AA:	

	Query Match	76.8%;	Score 622;	DB 18;	Length 113;
	Best Local Similarity	82.3%;	Pred. No. 1,01e-39;		
	Matches	93;	Conservative	7;	Mismatches 12; Indels 1; Gaps 1;
Db	1	dvvmtgslslpvtlqgpasiscrsqslvysdgnkylnwfgqrgqsprlllykvsnd	60		
QY	1	DVVMTQSPFLVLTGQPASISCRSSQSLHSGNGTYLNLWLQRCQSPQLIYLVSKLE	60		
Db	61	sgvpdrfsgsgsgtdftllksrrveaedvgvyvcmgthswtffggtkvvelk	113		
QY	61	SGVPDRFSGSGSGTDFTLLISG-VEAEDGVYVCMQFTHYPYTFGGTKLEIN	112		

QY 61 SGVPDRFSGSGSDTFLKISG-VEAEDVGYYCMQFTHYPVTFQGTKLEIK 112  
 RESULT 13  
 ID W48248 standard; Protein; 112 AA.

ID W48248 standard; Protein; 112 AA.  
AC W48248;  
DE 22-JUN-1998 (first entry)  
DT A77 anti-Fc alpha R antibody light chain variable V kappa region.  
KW A77 anti-Fc alpha R antibody; Fc-alpha receptor; antigen; cancer  
KW cytotoxic; white blood cell; infection.  
OS Synthetic.

DE A/7 anti-Fc alpha R antibody light chain variable Vkappa region.  
KW A77 anti-Fc alpha R antibody; Fc-alpha receptor; antigen; cancer  
KW cytotoxic; white blood cell; infection.  
OS Synthetic.

OS Homo sapiens.  
 PN WO9802453-A1.  
 PD 22-JAN-1998.  
 PF 10-JUL-1997; U12013.  
 PR 11-JUL-1996; US-678194.  
 PA (MEDA-) MEDAREX INC.  
 PI Deo YM, Graziano R, Keler T;  
 DR WPI: 98-110533/10.  
 DR N-PSDB; V20601.  
 PT Multispecific binding molecules reactive with Fc-alpha receptor and  
 PT antigen - for treatment and prevention of cancer and infections by  
 PT activating cytotoxic potential of Fc-alpha on white blood cells  
 PS Claim 18; Page 60; 106pp; English.  
 CC The present sequence represents A77 anti-Fc alpha R antibody light chain  
 CC variable V kappa region, which is used to produce the humanised  
 CC determinant in a bi-specific binding molecule of the present invention.  
 CC The present invention describes a bi- or multi-specific binding molecule  
 CC (I) comprising a first binding determinant (BD1) which binds a Fc alpha  
 CC receptor and a second BD (BD2) that binds to at least one antigen (Ag).  
 CC (I) are used: (i) to eliminate/reduce unwanted cells in a subject (human  
 CC or animal); (ii) to vaccinate against pathogens (specifically Candida  
 CC but many others disclosed including hepatitis and human immune  
 CC deficiency viruses); (iii) to arm effector cells against pathogens or  
 CC cancer cells. Ag may also be an allergen. (I) exploits the cytotoxic  
 CC (cytolytic and phagocytic) potential of Fc alpha on white blood cells,  
 CC improving their on cancer/infectious cells. When used in vaccines, (I) may  
 CC reduce the amount of antigen needed, and may be effective in patients  
 CC who do not respond well to antigen.  
 SQ Sequence 112 AA;

Query Match 76.58; Score 620; DB 29; Length 112;  
 Best Local Similarity 77.78; Pred. No. 1.47e-39;  
 Matches 87; Conservative 13; Mismatches 12; Indels 0; Gaps 0;  
 Db 1 digitqspstltstvgpafscsksgllsdgktnllwllqrgpsgptrllvskld 60  
 QY 1 DVVMTQSPPSLLVTLGQPASISCRSSGSLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60  
 Db 61 sgvpdrftgsgsgtdftlkisrveaedlgvycwggahfpqtfgggktleik 112  
 QY 61 SGVPDRFSGSGGTDFTLKISGVEADGVYICMQFTHYPTFGGQTKLEIK 112

RESULT 14  
 ID R12361 standard; Protein; 132 AA.  
 AC R12361;  
 DT 15-AUG-1991 (first entry)  
 DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.  
 KW Chimeric antibodies; immunocjugates; HIV; AIDS.  
 OS Mus musculus.  
 PN WO9107493-A.  
 PD 30-MAY-1991.  
 PF 13-NOV-1990; U06615.  
 PR 13-NOV-1989; US-433730.  
 PA (XOMA-) XOMA CORP.  
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;  
 DR WPI: 91-178044/24.  
 DR N-PSDB; Q12063.  
 PT New chimeric mouse-human antibodies - used to detect, kill and  
 PT remove HIV-1 antigen from sample  
 PS Disclosure; fig 18; 107pp; English.  
 CC This is the light (kappa) - chain variable (V) region of a mouse  
 CC monoclonal antibody (MAB), 4D12, and is specific for an HIV-1  
 CC viral antigen. It is used in the construction of a chimeric  
 CC MAB comprising heavy and light chains having murine V regions  
 CC and human C regions. The chimeric MABs are more effective than  
 CC murine MAB 4D12 since they have an increased compatibility in  
 CC humans. The heavy and light chain V-regions are joined by  
 CC manipulating their respective joining (J) regions, to generate  
 CC restriction enzyme recognition sites. The chimeric MABs can be  
 CC used as immunocjugates, in association with e.g. toxins for HIV  
 CC treatment. They can also be used in diagnosis of HIV.

CC See also Q12056-62.  
 SQ Sequence 132 AA;  
 Query Match 76.3%; Score 618; DB 2; Length 132;  
 Best Local Similarity 75.9%; Pred. No. 2.12e-39;  
 Matches 85; Conservative 16; Mismatches 11; Indels 0; Gaps 0;  
 Db 21 dvvmtqptltstvgpafscsksgllsdgktnllwllqrgpsgptrllvskld 80  
 QY 1 DVVMTQSPPSLLVTLGQPASISCRSSGSLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60  
 Db 81 sgvpdrftgsgsgtdftlkisrveaedlgvycwggahfpqtfgggktleir 132  
 QY 61 SGVPDRFSGSGGTDFTLKISGVEADGVYICMQFTHYPTFGGQTKLEIK 112

RESULT 15  
 ID R12239 standard; Protein; 131 AA.  
 AC R12239;  
 DT 19-AUG-1991 (first entry)  
 DE Mouse MAB 4D12 L chain V region.  
 KW HIV-1; Chimera.  
 OS Mus sp.  
 PN WO9107494-A.  
 PD 30-MAY-1991.  
 PF 13-NOV-1990; U06627.  
 PR 13-NOV-1989; US-433703.  
 PA (XOMA-) XOMA CORP.  
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;  
 DR WPI: 91-178106/24.  
 DR N-PSDB; Q12019.  
 PT New chimeric mouse human antibodies - used in treatment, diagnosis  
 PT and prophylaxis of HIV infections.  
 PS Disclosure; Fig 18; 108pp; English.  
 CC The mouse VL gene product may be used to produce chimeric mouse-  
 CC human Abs against HIV-1 comprising human Ig constant regions and  
 CC murine variable regions. These novel sequence are useful in  
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be  
 CC produced by a bacterial, yeast or mammalian expression system.  
 SQ Sequence 131 AA;

Query Match 75.8%; Score 614; DB 2; Length 131;  
 Best Local Similarity 76.6%; Pred. No. 4.45e-39;  
 Matches 85; Conservative 15; Mismatches 11; Indels 0; Gaps 0;  
 Db 21 dvvmtqptltstvgpafscsksgllsdgktnllwllqrgpsgptrllvskld 80  
 QY 1 DVVMTQSPPSLLVTLGQPASISCRSSGSLHSSGNTYLNWLLQRPQSPQLIYLVSKLE 60  
 Db 81 sgvpdrftgsgsgtdftlkisrveaedlgvycwggahfpqtfgggktlei 131  
 QY 61 SGVPDRFSGSGGTDFTLKISGVEADGVYICMQFTHYPTFGGQTKLEI 111

Search completed: Thu Jan 14 17:12:57 1999  
 Job time : 34 secs.



(TM)

1	655	76.5	118	2	S36265	Ig heavy chain v reg1	1.20e-80
2	653	76.3	135	2	S49530	anti-Sm antibody VH C	2.46e-80
3	613	71.6	123	2	D33348	Ig heavy chain V-l re	4.25e-74
4	592	69.2	116	2	S55342	Ig heavy chain v reg1	7.42e-71
5	584	68.2	121	2	S20783	Ig heavy chain v reg1	1.36e-69
6	583	68.1	138	2	S21810	Ig heavy chain v reg1	1.94e-69
7	582	68.0	246	2	S30950	Ig gamma chain - mous	2.78e-69
8	582	68.0	446	2	S40395	Ig gamma-2a chain (mA	2.78e-69
9	582	68.0	474	2	S25057	Ig gamma-2b chain - m	2.78e-69
10	581	67.9	110	2	PH1069	Ig heavy chain v reg1	3.97e-69
11	581	67.9	118	2	C30360	Ig heavy chain v reg1	3.97e-69
12	580	67.8	136	2	S31600	Ig heavy chain v reg1	5.67e-69
13	579	67.6	120	2	PH0362	Ig heavy chain v reg1	8.10e-69
14	577	67.4	120	2	B22769	Ig heavy chain v reg1	1.65e-68
15	577	67.4	131	2	A27472	Ig heavy chain v reg1	1.65e-68
16	577	67.4	139	2	PS0024	Ig heavy chain v reg1	1.65e-68
17	576	67.3	139	2	C30362	Ig heavy chain v reg1	2.36e-68
18	576	67.3	139	1	MHMS18	Ig heavy chain v reg1	2.36e-68
19	576	67.3	287	3	PC4402	haptan-specific singl	2.36e-68
20	575	67.2	142	2	A32483	Ig heavy chain v reg1	3.38e-68
21	574	67.1	104	2	S69899	Ig heavy chain v reg1	4.82e-68
22	574	67.1	117	2	D30269	PL7-6 antibody heavy	4.82e-68
23	573	66.9	119	2	JC3562	Ig heavy chain v reg1	6.89e-68



```

REFERENCE S48797
#authors Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
#submission submitted to the EMBL Data Library, October 1994
#description Molecular characterization of natural human anti-Sm
autoantibodies.
#accession S49530
#status preliminary
#molecule_type mRNA
#residues 1-135 #label MAH
#cross-references EMBL:Z46348; NID:g560839; PID:g560840
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE 34-117
#domain immunoglobulin homology #label IMM
SUMMARY #length 135 #molecular-weight 14997 #checksum 8132

Query Match 76.3%; Score 653; DB 2; Length 135;
Best Local Similarity 77.1%; Pred. No. 2.46e-80;
Matches 91; Conservative 10; Mismatches 15; Indels 2; Gaps 1;

Db 20 QVQLVQSGAEVKKPGASVKVSCKASGFTFTGYMHVWRQAPQGQLEWGMWNPNSGGTNY 79
|||||
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFTFTGYMHVWRQAPQGQLEWGMWNPNSGGTNY 60
|||||

Db 80 AOKFGQVTTTRDTSINTAYMELSRSLSDDTAVYVCARGFY--NYWGQGLTVTVSS 135
|||||
QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDDTAVYVCARGFNYRFAYWGQGLTVTVSS 118
|||||

RESULT 3
ENTRY D33548 #type complete
TITLE Ig heavy chain V-1 region (W1L2) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996

ACCESSIONS D33548
REFERENCE A33548
#authors Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chronic
lymphocytic leukemia.
#cross-references MIM:89345575
#accession D33548
#status preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
#molecule_type mRNA
#residues 1-123 #label KIP
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE heterotetramer; immunoglobulin
15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 123 #molecular-weight 13789 #checksum 9208

Query Match 71.6%; Score 613; DB 2; Length 123;
Best Local Similarity 73.2%; Pred. No. 4.25e-74;
Matches 90; Conservative 11; Mismatches 17; Indels 5; Gaps 2;

Db 1 QVQLVQSGAEVKKPGASVKVSCEASGFTFTGHVHWWRQAPQGQLEWGMWNPNSGGTNY 60
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QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFTFTGYMHVWRQAPQGQLEWGMWNPNSGGTNY 60
|||||

Db 61 AOKFGQVTTTRDTSINTAYMELSRSLSDDTAVYVCARGFYCGYDXYFFDYGQGLTVT 120
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QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDDTAVYVCARGF--N--YRFAYWGQGLTVT 115
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Db 121 VSS 123
QY 116 VSS 118

RESULT 4
ENTRY S55542 #type fragment

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```

TITLE Ig heavy chain V region pe2 - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
08-Sep-1997

ACCESSIONS S55542
REFERENCE S55528
#authors Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
#journal J. Mol. Biol. (1995) 247:932-946
#title Comprehensive epitope analysis of monoclonal
anti-proenkephalin antibodies using phage display libraries
and synthetic peptides: revelation of antibody fine
specificities caused by somatic mutations in the variable
region genes.
#accession S55542
#status preliminary
#molecule_type mRNA
#residues 1-116 #label BOE
#cross-references EMBL:X82581; NID:g854302; PID:g854303
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE heterotetramer; immunoglobulin
14-97
SUMMARY #domain immunoglobulin homology #label IMM
#length 116 #checksum 418

Query Match 69.2%; Score 592; DB 2; Length 116;
Best Local Similarity 70.1%; Pred. No. 7.80e-71;
Matches 82; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

Db 1 VQLQESGAELVKPGASVKLSCKASGYTFTRYMYWVWRQPGQLEWIGFINSNGTNN 60
|||||
QY 2 VQLQSGAEVKKPGASVKVSCKASGYTFTEYMYWVRQAPQGQLEWGRIDPDGSDIV 61
|||||

Db 61 EKFKSKATLVYDKSSSTAYMOLSSLTSDSAVYCTRGWA--SMDYWGQGLTVTVSS 116
|||||
QY 62 EKFKKKVTLTADTSSSTAYMELSSLTSDTAVYVCARGFNYRFAYWGQGLTVTVSS 118
|||||

RESULT 5
ENTRY S20783 #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997

ACCESSIONS S20783
REFERENCE S20764
#authors Mortari, F.; Wang, J.; Schroeder, H.W.
#submission submitted to the EMBL Data Library, April 1992
#description Analysis of human cord blood Ig heavy chain IgA and IgG
repertoire.
#accession S20783
#status preliminary
#molecule_type DNA
#residues 1-121 #label MOR
#cross-references EMBL:Z11957; NID:g33899; PID:g33900
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE heterotetramer; immunoglobulin
15-98
SUMMARY #length 121 #molecular-weight 13033 #checksum 8006

Query Match 68.2%; Score 584; DB 2; Length 121;
Best Local Similarity 68.6%; Pred. No. 1.36e-69;
Matches 83; Conservative 13; Mismatches 22; Indels 3; Gaps 2;

Db 1 QVQLVQSGAEVKKPGASVTVSKASGYTFTFYFHWWRQAPQGQLEWGMWNPNSGGTTF 60
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QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTFYMYWVRQAPQGQLEWGRIDPDGSDIV 60
|||||

Db 61 AOKLQGRATVTRDTSSTVYMDLSRSEDITAYVCARGSDTSPASTIDYWGQGLTVTVS 120
|||||
QY 61 VERFKKKVTLTADTSSSTAYMELSSLTSDTAVYVCARG--KF-NYRFAYWGQGLTVTVS 117
|||||

Db 121 S 121
QY 118 S 118

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6
RESULT      S21810      #type complete
ENTRY      Ig heavy chain V region - mouse
TITLE      #formal_name Mus musculus #common_name house mouse
ORGANISM   20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
DATE       08-Sep-1997
ACCESSIONS S21810
REFERENCE  Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
#authors   submitted to the EMBL Data Library, January 1991
#description Nucleotide sequence of a rearranged VDJ-region of a mouse Ig
            mu heavy chain gene and its upstream region.
#accession S21810
#status    preliminary
#molecule_type DNA
#residues  1-138 #label OST
#cross-references EMBL:X56936; NID:g54163; RID:g54164.
GENETICS
#introns   15/3
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
FEATURE
34-117      #domain immunoglobulin homology #label IMM
SUMMARY      #length 138 #molecular-weight 15258 #checksum 1535
Query Match  68.1%; Score 583; DB 2; Length 138;
Best Local Similarity 68.9%; Pred. No. 1.94e-69;
Matches 82; Conservative 17; Mismatches 19; Indels 1; Gaps 1;
Db 20 QVQLQSGPELVPGASVRSICRSGYFTFTSYIHVWKQPGGLEWIGWYGNVNTKY 79
QY 1 QVQLVQSGAEVKKPGASVKVCARSGYFTFTSYIMYVRQAPGQLEMLGRDPEDGSIDY 60
Db 80 NEKFKGKATLTADKSSATYMWOLSSLTSEDYAVYFCARGG-KFANDYWGQGTSTVTS 138
QY 61 VERFKKVTLTADTSSSTAYMELSSLTSDTAVYICARG-KFNRYFAYWGQGTSTVTS 118

7
RESULT      S38950      #type complete
ENTRY      Ig gamma chain - mouse
TITLE      #formal_name Mus musculus #common_name house mouse
ORGANISM   19-May-1994 #sequence_revision 10-Nov-1995 #text_change
DATE       23-May-1997
ACCESSIONS S38950
REFERENCE  Kleibert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.;
#authors   Frosch, M.; Weisgerber, C.; Bitter-Suermann, D.;
            Hilschmann, N.
#journal   Biol. Chem. Hoppe-Seyler (1993) 374:993-1000
#title     Primary structure of the murine monoclonal IgG2a antibody
            mAb735 against alpha(2-8) polysialic acid. 2. Amino acid
            sequence of the heavy (H-)chain Fd' region.
#accession S38950
#status    preliminary
#molecule_type protein
#residues  1-246 #label KLE
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS     immunoglobulin
FEATURE
137-201     #domain immunoglobulin homology #label IGG1
SUMMARY      #length 246 #molecular-weight 26216 #checksum 7059
Query Match  68.0%; Score 582; DB 2; Length 246;
Best Local Similarity 67.8%; Pred. No. 2.78e-69;
Matches 80; Conservative 18; Mismatches 19; Indels 1; Gaps 1;
Db 1 QIQLQSGPELVPGASVKISCKASGYFTFDYIHVWKQPGGLEWIGWYPGSGNTKY 60
QY 1 QVQLVQSGAEVKKPGASVKVCARSGYFTFTSYIMYVRQAPGQLEMLGRDPEDGSIDY 60

9
RESULT      S25057      #type complete
ENTRY      Ig gamma-2b chain - mouse
TITLE      #formal_name Mus musculus #common_name house mouse
ORGANISM   19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
DATE       31-Oct-1997
ACCESSIONS S25057
REFERENCE  Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch,
#authors   H.J.; Kreuzaler, F.
            submitted to the EMBL Data Library, July 1992
#submission

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Db 61 NEKFKGKATLTVDTSSTAYMOLSSLTSEDYAVYFCARGG-KFANDYWGQGTSTVTS 117
QY 61 VERFKKVTLTADTSSSTAYMELSSLTSDTAVYICARGKFNRYFAYWGQGTSTVTS 118

8
RESULT      S40295      #type complete
ENTRY      Ig gamma-2a chain (mAb735) - mouse
TITLE      #formal_name Mus musculus #common_name house mouse
ORGANISM   07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
DATE       23-May-1997
ACCESSIONS S40295
REFERENCE  Kleibert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.;
#authors   Frosch, M.; Weisgerber, C.; Bitter-Suermann, D.;
            Hilschmann, N.
#submission submitted to the EMBL Data Library, January 1993
#description Primary structure of the murine monoclonal IgG2a antibody
            mAb735 against (2-8) polysialic acid. 2. Amino acid
            sequence of the heavy (H-) chain Fd' region.
#accession S40295
#molecule_type protein
#residues  1-446 #label KLE
GENETICS
#map_position 12
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS     disulfide bond; glycoprotein; immunoglobulin; pyroglutamic
            acid
FEATURE
1-446       #product Ig gamma-2a chain #status experimental #label
            MAT
1-117       #domain V-D-J region #label VDJ\
118-446     #domain C region #label CHR\
118-214     #domain C1 region #label CH1\
215-230     #region hinge\
231-340     #domain C2 region #label CH2\
341-446     #domain C3 region #label CH3\
360-427     #domain immunoglobulin homology #label IGG3\
1           #modified_site pyrrolidone carboxylic acid (Gln) #status
            experimental\
22-96,144-199,
261-321,367-425
132         #disulfide_bonds #status predicted\
            #disulfide_bonds interchain (to light chain) #status
            predicted\
224,227,229 #disulfide_bonds interchain #status predicted\
297         #binding_site carbohydrate (Asn) (covalent) #status
            experimental
SUMMARY      #length 446 #molecular-weight 49108 #checksum 6356
Query Match  68.0%; Score 582; DB 2; Length 446;
Best Local Similarity 67.8%; Pred. No. 2.78e-69;
Matches 80; Conservative 18; Mismatches 19; Indels 1; Gaps 1;
Db 1 QIQLQSGPELVPGASVKISCKASGYFTFDYIHVWKQPGGLEWIGWYPGSGNTKY 60
QY 1 QVQLVQSGAEVKKPGASVKVCARSGYFTFTSYIMYVRQAPGQLEMLGRDPEDGSIDY 60

9
RESULT      S25057      #type complete
ENTRY      Ig gamma-2b chain - mouse
TITLE      #formal_name Mus musculus #common_name house mouse
ORGANISM   19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
DATE       31-Oct-1997
ACCESSIONS S25057
REFERENCE  Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch,
#authors   H.J.; Kreuzaler, F.
            submitted to the EMBL Data Library, July 1992
#submission

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#description Production of a Tobacco mosaic virus (TMV) inactivating  
neotop specific monoclonal antibody in Nicotiana tabacum.

#accession S25057  
#status preliminary  
#molecule\_type mRNA  
#residues 1-474 #label FTS  
#cross-references EMBL:457210; NID:954826; PID:954827  
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology  
SUMMARY #length 474 #molecular-weight 52069 #checksum 4891

Query Match 68.0%; Score 582; DB 2; Length 474;  
Best Local Similarity 67.2%; Pred. No. 2,78e-69;  
Matches 80; Conservative 19; Mismatches 18; Indels 2; Gaps 2;

Db 20 EVQLQSGPELVNPGASVKMSCKASGYTFITYMHVWVKRPGQGLEWIGYINPNKDKGTF 79

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTEYIMYWRQAPQGQLEMLGRIDPEDGSIDY 60

Db 80 NEKFKGKATLTSSNTAYMELSLTSDSAVYYCARD-YDYDFWFGQGLTVTVSSA 137

QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYCARGFNY-RFAYWGQGLTVTVSS 118

RESULT 10  
ENTRY  
TITLE Ig heavy chain V region (clone 3B2) - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change  
16-Aug-1996

ACCESSIONS PH1669  
REFERENCE PH1642  
#authors Hillison, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

#journal J. Exp. Med. (1993) 178:331-336  
#title The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A.

#accession PH1669  
#molecule\_type mRNA  
#residues 1-110 #label HIL  
#experimental\_source B cell  
#superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotrimer; immunoglobulin

FEATURE 7-90  
SUMMARY #domain immunoglobulin homology #label IMM  
#length 110 #checksum 8449

Query Match 67.9%; Score 581; DB 2; Length 110;  
Best Local Similarity 72.7%; Pred. No. 3,97e-69;  
Matches 80; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Db 1 AEVKKPGASVKVSKASGYTFITYMHVWVRQAPQGQLEWGRINANSQGTNYAQRQGRV 60

QY 9 AEVKKPGASVKVSKASGYTFITYMHVWVRQAPQGQLEMLGRIDPEDGSIDYVEKFKKV 68

Db 61 TMTRDTSTAYMELSLRSEDVAVYCARDLTGDAFWIGQGLTVTVSS 110

QY 69 TLTDSTSSSTAYMELSLTSDTAVYCARGFNYRFAYWGQGLTVTVSS 118

RESULT 11  
ENTRY  
TITLE Ig heavy chain V region (35.8.2H) - mouse (fragment)  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 23-Mar-1989 #sequence\_revision 03-Aug-1992 #text\_change  
20-Mar-1998

ACCESSIONS C30560  
REFERENCE A30560  
#authors Matsuda, T.; Kabat, E.A.  
#journal J. Immunol. (1989) 142:863-870  
#title Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1->6)dextran.

#cross-references MUID:89110062

#accession C30560

#status preliminary

#molecule\_type mRNA

#residues 1-118 #label MAT

#cross-references GB:M24270; NID:9195615; PID:9195616

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS heterotrimer; immunoglobulin

FEATURE 15-98

SUMMARY #domain immunoglobulin homology #label IMM  
#length 118 #checksum 9448

Query Match 67.9%; Score 581; DB 2; Length 118;

Best Local Similarity 68.9%; Pred. No. 3,97e-69;

Matches 82; Conservative 16; Mismatches 19; Indels 2; Gaps 2;

Db 1 QVHLQSGAEVKKPGASVKISCKASGYTFITYMHVWVRQAPQGQLEWIGEDIPSNSTYN 60

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFITYMYWRQAPQGQLEMLGRIDPEDGSIDY 60

Db 61 NQFKNKATLVKSSNTAYMQLSLTSDSAVYYCARWGT-GSWFAYWGQGLTVTVSSA 118

QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYCAR-GKFNRYFAYWGQGLTVTVSS 118

RESULT 12

ENTRY

TITLE Ig heavy chain V region - human (fragment)

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change  
08-Sep-1997

ACCESSIONS S31600

REFERENCE S31585

#authors Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;

#submission Tonnel, C.

#description submitted to the EMBL Data Library, June 1992

#accession S31600

#status preliminary

#molecule\_type mRNA

#residues 1-136 #label CUI

#cross-references EMBL:214165; NID:930994; PID:930995

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS heterotrimer; immunoglobulin

FEATURE 34-117

SUMMARY #domain immunoglobulin homology #label IMM  
#length 136 #checksum 9862

Query Match 67.8%; Score 580; DB 2; Length 136;

Best Local Similarity 70.3%; Pred. No. 5,67e-69;

Matches 83; Conservative 15; Mismatches 18; Indels 2; Gaps 2;

Db 20 QVQLVQSGAEVKKPGASVKVSKASGYTFITYDINVRQATQGQLEWGMNPSGNTGY 79

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFITYMYWRQAPQGQLEMLGRIDPEDGSIDY 60

Db 80 AQKQGRVTMTNYSISTAYMELSLRSEDVAVYCARWR-D-AFDWGQGLTVTVSS 135

QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYCARGFNYRFAYWGQGLTVTVSS 118

RESULT 13

ENTRY

TITLE Ig heavy chain V region (G6+ T-L42) - human (fragment)

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change  
16-Aug-1996

ACCESSIONS PH0962

REFERENCE PH0952

#authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

#journal J. Exp. Med. (1992) 175:983-991

#title Evidence for somatic selection of natural autoantibodies.

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RESULT 15
ENTRY Ig heavy chain precursor V region (1E9) - mouse (fragment)
TITLE #formal_name Mus musculus #common_name house mouse
ORGANISM 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
DATE 18-Oct-1996
ACCESSIONS A27472
REFERENCE A27472
#authors Liu, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.
#journal Gene (1987) 54:33-40
#title Expression of mouse:human immunoglobulin heavy-chain cDNA in lymphoid cells.
#cross-references MUID:87277430
#accession A27472
#molecule_type mRNA
#residues 1-131 #label LIU
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
FEATURE
1-19 #domain signal sequence #status predicted #label SIG\
5-54 #region complementarity-determining 1\
20-131 #product Ig heavy chain V region 1E9 #status predicted
#label MAT\
34-117 #domain immunoglobulin homology #label IMM\
69-85 #region complementarity-determining 2\
118-125 #region complementarity-determining 3
SUMMARY
#length 131 #checksum 1501
Query Match 67.4%; Score 577; DB 2; Length 131;
Best Local Similarity 69.3%; Pred. No. 1,85e-68;
Matches 79; Conservative 16; Mismatches 16; Indels 3; Gaps 3;
Db 20 QVQLQPGAEIVKPGASVKLSKASGYTFTSYMHVVKRPGQGLDWIGEINPSNGRTNY 79
QY 1 QVQLVQSGAEVKPGASVKVSCRASGYTFTSYMYVVRQAPGQGLMGRIPDEGSIDY 60
Db 80 NEFKSKATLTVDKSSSTAYMQLSSITSEDSAVYYCA-S-YDYDFAYWGQGTFL 131
QY 61 VEKFFKKRTLTADTSSTAYMELSSLTSDTAVYYCARGKFN-REAYWGQGTFL 113

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Search completed: Thu Jan 14 17:14:47 1999  
Job time : 17 secs.

(TM)

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	576	67.3	139	1 HV07_MOUSE	IG HEAVY CHAIN PRECURS	2.56e-100
2	571	66.7	118	1 HV51_MOUSE	IG HEAVY CHAIN V REGIO	3.66e-100
3	569	66.5	117	1 HV13_MOUSE	IG HEAVY CHAIN V REGIO	1.06e-100
4	568	66.4	138	1 HV48_MOUSE	IG HEAVY CHAIN PRECURS	1.81e-100
5	567	66.2	137	1 HV11_MOUSE	IG HEAVY CHAIN PRECURS	3.07e-100
6	565	66.1	117	1 HV1G_HUMAN	IG HEAVY CHAIN PRECURS	5.23e-100
7	566	66.0	117	1 HV1B_HUMAN	IG HEAVY CHAIN PRECURS	8.89e-100
8	565	65.0	117	1 HV12_MOUSE	IG HEAVY CHAIN V REGIO	1.06e-98
9	541	63.2	120	1 HV50_MOUSE	IG HEAVY CHAIN V REGIO	3.00e-95
10	539	63.0	140	1 HV02_MOUSE	IG HEAVY CHAIN PRECURS	8.66e-95
11	521	60.9	117	1 HV09_MOUSE	IG HEAVY CHAIN PRECURS	1.18e-90
12	520	60.7	120	1 HV03_MOUSE	IG HEAVY CHAIN V REGIO	1.99e-90
13	513	59.9	117	1 HV04_MOUSE	IG HEAVY CHAIN PRECURS	8.00e-89
14	511	59.7	117	1 HV06_MOUSE	IG HEAVY CHAIN PRECURS	2.30e-88
15	505	59.0	117	1 HV10_MOUSE	IG HEAVY CHAIN PRECURS	5.41e-87
16	503	58.8	114	1 HV00_MOUSE	IG HEAVY CHAIN V REGIO	1.55e-86
17	503	58.8	143	1 HV1C_HUMAN	IG HEAVY CHAIN PRECURS	1.55e-86
18	500	58.4	117	1 HV49_MOUSE	IG HEAVY CHAIN PRECURS	7.52e-86
19	490	57.2 <sup>a</sup>	136	1 HV15_MOUSE	IG HEAVY CHAIN PRECURS	1.44e-83
20	489	57.1	117	1 HV05_MOUSE	IG HEAVY CHAIN PRECURS	2.44e-83
21	487	56.9	117	1 HV52_MOUSE	IG HEAVY CHAIN PRECURS	6.96e-83
22	484	56.5	117	1 HV14_MOUSE	IG HEAVY CHAIN PRECURS	3.36e-82
23	480	56.1	121	1 HV01_MOUSE	IG HEAVY CHAIN V REGIO	2.74e-81

QY	1	QVOLVOSGAEVKPKGASVKSCASGYTTEYYMYWRAOPGGGLEMGRLDPDGSIDY	60																																																																																																																																																						
Db	61	NOKFKKATILTVDKSSSTAYMOLNSLTSSEDSAVYYCARDRIWY-FDVMGAGTWTVTYSS	117																																																																																																																																																						
QY	61	VEKFKKKVTLTADTSSTAYMELSSLTSDTAVYYCARGKFNRYFAYWGQGLTVTVSS	118																																																																																																																																																						
<p>RESULT 4</p> <table border="0"> <tr> <td>ID</td><td>HV48_MOUSE</td><td>STANDARD;</td><td>PRT;</td><td>138 AA.</td></tr> <tr> <td>AC</td><td>P03980;</td><td></td><td></td><td></td></tr> <tr> <td>DT</td><td>23-OCT-1986</td><td>(REL. 02, CREATED)</td><td></td><td></td></tr> <tr> <td>DT</td><td>23-OCT-1986</td><td>(REL. 02, LAST SEQUENCE UPDATE)</td><td></td><td></td></tr> <tr> <td>DT</td><td>01-AUG-1992</td><td>(REL. 23, LAST ANNOTATION UPDATE)</td><td></td><td></td></tr> <tr> <td>DE</td><td>IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).</td><td></td><td></td><td></td></tr> <tr> <td>DE</td><td>MUS MUSCULUS (MOUSE).</td><td></td><td></td><td></td></tr> <tr> <td>OC</td><td>EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;</td><td></td><td></td><td></td></tr> <tr> <td>OC</td><td>EUTHERIA; RODENTIA.</td><td></td><td></td><td></td></tr> <tr> <td>RN</td><td>[1]</td><td></td><td></td><td></td></tr> <tr> <td>RN</td><td>SEQUENCE FROM N.A.</td><td></td><td></td><td></td></tr> <tr> <td>RP</td><td>MEDLINE; 84248078.</td><td></td><td></td><td></td></tr> <tr> <td>RX</td><td>GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,</td><td></td><td></td><td></td></tr> <tr> <td>RA</td><td>TUCKER P.W.;</td><td></td><td></td><td></td></tr> <tr> <td>RL</td><td>PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).</td><td></td><td></td><td></td></tr> <tr> <td>DR</td><td>PIR; A02033; HVMST7.</td><td></td><td></td><td></td></tr> <tr> <td>DR</td><td>HSP; P01810; 1JHL.</td><td></td><td></td><td></td></tr> <tr> <td>DR</td><td>IMMUNOGLOBULIN V REGION; SIGNAL.</td><td></td><td></td><td></td></tr> <tr> <td>KW</td><td>SIGNAL</td><td>1</td><td>20</td><td></td></tr> <tr> <td>FT</td><td>CHAIN</td><td>21</td><td>138</td><td>IG HEAVY CHAIN V REGION (TEPC 1017).</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>21</td><td>49</td><td>FRAMEWORK 1.</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>50</td><td>54</td><td>COMPLEMENTARITY-DETERMINING 1.</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>55</td><td>68</td><td>FRAMEWORK 2.</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>69</td><td>85</td><td>COMPLEMENTARITY-DETERMINING 2.</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>86</td><td>117</td><td>FRAMEWORK 3.</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>118</td><td>127</td><td>COMPLEMENTARITY-DETERMINING 3.</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>128</td><td>138</td><td>FRAMEWORK 4.</td></tr> <tr> <td>FT</td><td>DISULFID</td><td>41</td><td>115</td><td>BY SIMILARITY.</td></tr> <tr> <td>FT</td><td>NON_TER</td><td>138</td><td>138</td><td></td></tr> <tr> <td>SEQ</td><td>SEQUENCE</td><td>138 AA;</td><td>15576 MW;</td><td>BEF6247B CRC32;</td></tr> </table> <p>Query Watch 66.4%; Score 568; DB 1; Length 138;  Best Local Similarity 66.4%; Pred. No. 1.8ie-101;  Matches 79; Conservative 18; Mismatches 21; Indels 1; Gaps 1</p>				ID	HV48_MOUSE	STANDARD;	PRT;	138 AA.	AC	P03980;				DT	23-OCT-1986	(REL. 02, CREATED)			DT	23-OCT-1986	(REL. 02, LAST SEQUENCE UPDATE)			DT	01-AUG-1992	(REL. 23, LAST ANNOTATION UPDATE)			DE	IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).				DE	MUS MUSCULUS (MOUSE).				OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				OC	EUTHERIA; RODENTIA.				RN	[1]				RN	SEQUENCE FROM N.A.				RP	MEDLINE; 84248078.				RX	GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,				RA	TUCKER P.W.;				RL	PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).				DR	PIR; A02033; HVMST7.				DR	HSP; P01810; 1JHL.				DR	IMMUNOGLOBULIN V REGION; SIGNAL.				KW	SIGNAL	1	20		FT	CHAIN	21	138	IG HEAVY CHAIN V REGION (TEPC 1017).	FT	DOMAIN	21	49	FRAMEWORK 1.	FT	DOMAIN	50	54	COMPLEMENTARITY-DETERMINING 1.	FT	DOMAIN	55	68	FRAMEWORK 2.	FT	DOMAIN	69	85	COMPLEMENTARITY-DETERMINING 2.	FT	DOMAIN	86	117	FRAMEWORK 3.	FT	DOMAIN	118	127	COMPLEMENTARITY-DETERMINING 3.	FT	DOMAIN	128	138	FRAMEWORK 4.	FT	DISULFID	41	115	BY SIMILARITY.	FT	NON_TER	138	138		SEQ	SEQUENCE	138 AA;	15576 MW;	BEF6247B CRC32;
ID	HV48_MOUSE	STANDARD;	PRT;	138 AA.																																																																																																																																																					
AC	P03980;																																																																																																																																																								
DT	23-OCT-1986	(REL. 02, CREATED)																																																																																																																																																							
DT	23-OCT-1986	(REL. 02, LAST SEQUENCE UPDATE)																																																																																																																																																							
DT	01-AUG-1992	(REL. 23, LAST ANNOTATION UPDATE)																																																																																																																																																							
DE	IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).																																																																																																																																																								
DE	MUS MUSCULUS (MOUSE).																																																																																																																																																								
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;																																																																																																																																																								
OC	EUTHERIA; RODENTIA.																																																																																																																																																								
RN	[1]																																																																																																																																																								
RN	SEQUENCE FROM N.A.																																																																																																																																																								
RP	MEDLINE; 84248078.																																																																																																																																																								
RX	GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,																																																																																																																																																								
RA	TUCKER P.W.;																																																																																																																																																								
RL	PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).																																																																																																																																																								
DR	PIR; A02033; HVMST7.																																																																																																																																																								
DR	HSP; P01810; 1JHL.																																																																																																																																																								
DR	IMMUNOGLOBULIN V REGION; SIGNAL.																																																																																																																																																								
KW	SIGNAL	1	20																																																																																																																																																						
FT	CHAIN	21	138	IG HEAVY CHAIN V REGION (TEPC 1017).																																																																																																																																																					
FT	DOMAIN	21	49	FRAMEWORK 1.																																																																																																																																																					
FT	DOMAIN	50	54	COMPLEMENTARITY-DETERMINING 1.																																																																																																																																																					
FT	DOMAIN	55	68	FRAMEWORK 2.																																																																																																																																																					
FT	DOMAIN	69	85	COMPLEMENTARITY-DETERMINING 2.																																																																																																																																																					
FT	DOMAIN	86	117	FRAMEWORK 3.																																																																																																																																																					
FT	DOMAIN	118	127	COMPLEMENTARITY-DETERMINING 3.																																																																																																																																																					
FT	DOMAIN	128	138	FRAMEWORK 4.																																																																																																																																																					
FT	DISULFID	41	115	BY SIMILARITY.																																																																																																																																																					
FT	NON_TER	138	138																																																																																																																																																						
SEQ	SEQUENCE	138 AA;	15576 MW;	BEF6247B CRC32;																																																																																																																																																					
Db	20	QVOLQOPGALVKPKGASVOLSCASGHTTNTYHWKORPGOGLEWIGENPDGRSNY	79																																																																																																																																																						
QY	1	QVOLVOSGAEVKPKGASVKSCASGYTTEYYMYWRAOPGGGLEMGRLDPDGSIDY	60																																																																																																																																																						
Db	80	NEKFNKATILTVDKSSSTAYMOLSSLTPEEFAYVYCARSDGYDWFVYWGQGLTVTFS	138																																																																																																																																																						
QY	61	VEKFKKKVTLTADTSSTAYMELSSLTSDTAVYYCARGKFNRYFAYWGQGLTVTVSS	118																																																																																																																																																						
<p>RESULT 5</p> <table border="0"> <tr> <td>ID</td><td>HV11_MOUSE</td><td>STANDARD;</td><td>PRT;</td><td>137 AA.</td></tr> <tr> <td>AC</td><td>P01755;</td><td></td><td></td><td></td></tr> <tr> <td>DT</td><td>21-JUL-1986</td><td>(REL. 01, CREATED)</td><td></td><td></td></tr> <tr> <td>DT</td><td>21-JUL-1986</td><td>(REL. 01, LAST SEQUENCE UPDATE)</td><td></td><td></td></tr> <tr> <td>DT</td><td>01-OCT-1996</td><td>(REL. 34, LAST ANNOTATION UPDATE)</td><td></td><td></td></tr> <tr> <td>DE</td><td>IG HEAVY CHAIN PRECURSOR V REGION (S43).</td><td></td><td></td><td></td></tr> <tr> <td>DE</td><td>MUS MUSCULUS (MOUSE).</td><td></td><td></td><td></td></tr> <tr> <td>OC</td><td>EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;</td><td></td><td></td><td></td></tr> <tr> <td>OC</td><td>EUTHERIA; RODENTIA.</td><td></td><td></td><td></td></tr> <tr> <td>RN</td><td>[1]</td><td></td><td></td><td></td></tr> <tr> <td>RN</td><td>SEQUENCE FROM N.A.</td><td></td><td></td><td></td></tr> <tr> <td>RX</td><td>MEDLINE; 81234548.</td><td></td><td></td><td></td></tr> <tr> <td>RX</td><td>BOTSWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESWY K.,</td><td></td><td></td><td></td></tr> <tr> <td>RA</td><td>BALTIMORE D.;</td><td></td><td></td><td></td></tr> <tr> <td>RL</td><td>CELL 24:625-637(1981).</td><td></td><td></td><td></td></tr> <tr> <td>CC</td><td>-!- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING</td><td></td><td></td><td></td></tr> <tr> <td>CC</td><td>ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB</td><td></td><td></td><td></td></tr> <tr> <td>CC</td><td>CC</td><td></td><td></td><td></td></tr> <tr> <td>DR</td><td>EMBL; J00539; G195119; -.</td><td></td><td></td><td></td></tr> <tr> <td>DR</td><td>PIR; A02038; G2MS43.</td><td></td><td></td><td></td></tr> </table>				ID	HV11_MOUSE	STANDARD;	PRT;	137 AA.	AC	P01755;				DT	21-JUL-1986	(REL. 01, CREATED)			DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)			DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)			DE	IG HEAVY CHAIN PRECURSOR V REGION (S43).				DE	MUS MUSCULUS (MOUSE).				OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				OC	EUTHERIA; RODENTIA.				RN	[1]				RN	SEQUENCE FROM N.A.				RX	MEDLINE; 81234548.				RX	BOTSWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESWY K.,				RA	BALTIMORE D.;				RL	CELL 24:625-637(1981).				CC	-!- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING				CC	ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB				CC	CC				DR	EMBL; J00539; G195119; -.				DR	PIR; A02038; G2MS43.																																																					
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DR	EMBL; J00539; G195119; -.																																																																																																																																																								
DR	PIR; A02038; G2MS43.																																																																																																																																																								

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DR HSP: P01772; LFV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION (S43).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 20 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 58 FRAMEWORK 2.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; C37539BD CRC32;

Query Match 66.28; Score 567; DB 1; Length 137;
Best Local Similarity 68.18; Pred. No. 3.07e-101;
Matches 81; Conservative 14; Mismatches 22; Indels 2; Gaps 2;

Db 20 QVQLVQSGAEVFKPGASVKSLCKASGTYFTSYLHMVWNPQPGGLEWGRINPNSGGTTY 79
QY 1 QVQLVQSGAEVFKPGASVKSLCKASGTYFTSYLHMVWNPQPGGLEWGRINPNSGGTTY 79
Db 80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYCYARYLGRY-FDYWGQGTLLTVSS 137
QY 61 VEKFKKVTLTADTSSSTAYMELSSLTSDTAVYCYARGKEN-YRFAYWGQGTLLTVSS 118

RESULT 6
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (V35).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88296408.
RA MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.,
RA OHNO H., FUKUHARA S., HONJO T.;
RL EMBO J. 7:1047-1051(1988).
DR EMBL; X07448; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR HSP; P01810; LFVB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; FAA560D1 CRC32;

Query Match 66.18; Score 566; DB 1; Length 117;
Best Local Similarity 79.68; Pred. No. 5.23e-101;
Matches 78; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Db 20 QVQLVQSGAEVFKPGASVKSLCKASGTYFTSYLHMVWNPQPGGLEWGRINPNSGGTTY 79
QY 1 QVQLVQSGAEVFKPGASVKSLCKASGTYFTSYLHMVWNPQPGGLEWGRINPNSGGTTY 79
Db 80 AQKFGQVTRTSTSTAYMELSSLTSDTAVYCYAR 117
QY 61 VEKFKKVTLTADTSSSTAYMELSSLTSDTAVYCYAR 98

RESULT 7
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (HG3).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88296408.
RA MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.,
RA OHNO H., FUKUHARA S., HONJO T.;
RL EMBO J. 7:1047-1051(1988).
DR EMBL; X07448; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR HSP; P01810; LFVB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; FAA560D1 CRC32;

Query Match 66.18; Score 566; DB 1; Length 117;
Best Local Similarity 79.68; Pred. No. 5.23e-101;
Matches 78; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Db 20 QVQLVQSGAEVFKPGASVKSLCKASGTYFTSYLHMVWNPQPGGLEWGRINPNSGGTTY 79
QY 1 QVQLVQSGAEVFKPGASVKSLCKASGTYFTSYLHMVWNPQPGGLEWGRINPNSGGTTY 79
Db 80 AQKFGQVTRTSTSTAYMELSSLTSDTAVYCYAR 117
QY 61 VEKFKKVTLTADTSSSTAYMELSSLTSDTAVYCYAR 98

RESULT 8
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN V REGION (MOPC 104E).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 83075344.
RA KERRY M.R., FUHRMAN J.S., SCHILLING J.W., ROGERS J., SIBLEY C.H.,
RA HOOD L.E.;
RL BIOCHEMISTRY 21:5415-5424(1982).
CC -|- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS
CC ALSO BEEN DETERMINED.
CC -|- THIS PROTEIN BINDS DEXTRAN.
DR HSP; P01772; LFV.
DR PIR; A02039; MHMS4E.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 1F6CC304 CRC32;

Query Match 65.08; Score 556; DB 1; Length 117;
Best Local Similarity 64.48; Pred. No. 1.06e-98;
Matches 76; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

Db 1 EVQLVQSGAEVFKPGASVKSLCKASGTYFTSYLHMVWNPQPGGLEWGRINPNSGGTTY 60
QY 1 EVQLVQSGAEVFKPGASVKSLCKASGTYFTSYLHMVWNPQPGGLEWGRINPNSGGTTY 60
Db 61 NOKEFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYCYAR-YDWTYFDVWGQGTLLTVSS 117
QY 61 VEKFKKVTLTADTSSSTAYMELSSLTSDTAVYCYARGKEN-YRFAYWGQGTLLTVSS 118

RESULT 9
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;

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DT 01-JAN-1988 (REL. 06, CREATED)  
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)  
 DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN V REGION (AC38 15.3).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 84182519.  
 RA DILDROP R., BOVENS J., SIEKEVITZ M., BEYREUTHER K., RAJEWSKY K.;  
 RL EMBO J. 3:517-523(1984).  
 DR PIR: A02037; MMS15.  
 DR HSP: P01772; IFGV.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 98 V SEGMENT.  
 FT DOMAIN 99 105 D SEGMENT.  
 FT DOMAIN 106 120 J SEGMENT.  
 FT DISULFID 22 96 BY SIMILARITY.  
 FT NON\_TER 120 120  
 SQ SEQUENCE 120 AA; 13311 MW; 85EC01BA CRC32;  
  
 Query Match 63.2%; Score 541; DB 1; Length 120;  
 Best Local Similarity 63.3%; Pred. No. 3,00e-95;  
 Matches 76; Conservative 20; Mismatches 22; Indels 2; Gaps 2;  
  
 Db 1 QVQLQPGTELVKPGASVNLSCASGYFTFTSYMMHWIRQPGQGLWIGINPNSGGTNY 60  
 QY 1 QVQLVQSGAEVKKPKASVKVCKASGYFTFTSYMMHWVQAPGQGLMGRIDPDGSDY 60  
  
 Db 61 NEKFKSKATLVKSSATYQWLTPTSDSNAVYCARWDYDGRYFDVWGTTGVTVSS-120  
 QY 61 VEKFKKVTLTADTSSPAYMELSLTSDTAVYCARGFN-YR-FAYWGQGLTVTVSS 118  
  
 RESULT 10  
 ID HV02\_MOUSE STANDARD; PRT; 140 AA.  
 AC P01746;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A/J;  
 RX MEDLINE; 82152818.  
 RA SIMS J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,  
 RA CAPRA J.D.;  
 RL SCIENCE 216:309-311(1982).  
 DR EMBL: J00493; G195007;  
 DR PIR: A02028; HYMSG7.  
 DR HSP: P01789; 6FAB.  
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA; SIGNAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).  
 FT NON\_TER 140 140  
 SQ SEQUENCE 140 AA; 15514 MW; 0700D5C8 CRC32;  
  
 Query Match 63.0%; Score 539; DB 1; Length 140;  
 Best Local Similarity 64.5%; Pred. No. 8.66e-95;  
 Matches 78; Conservative 20; Mismatches 20; Indels 3; Gaps 1;  
  
 Db 20 EVQLQQSGAEVLVGRAGSSVYKMSCKASGYFTFTSYGNNVKKQPGQGLWIGINPNSGGTNY 79  
 QY 1 QVQLVQSGAEVKKPKASVKVCKASGYFTFTSYMMHWVQAPGQGLMGRIDPDGSDY 60  
  
 Db 80 NEKFKGKTLTVKSSATYQWLTPTSDSNAVYCARSHYGGSDYFDYWGQGTPLTVS 139  
 QY 61 VEKFKKVTLTADTSSPAYMELSLTSDTAVYCARGFN-YR-FAYWGQGLTVTVS 117

Db 140 S 140  
 QY 118 S 118  
  
 RESULT 11  
 ID HV09\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01753; F11271;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (186-1).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6;  
 RX MEDLINE; 81234548.  
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,  
 RA BALTIMORE D.;  
 RL CELL 24:625-637(1981).  
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES  
 CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
 CC PIR: B02034; HYMSG1.  
 DR HSP: P01810; IFVB.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (186-1).  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12890 MW; C97683A2 CRC32;  
  
 Query Match 60.9%; Score 521; DB 1; Length 117;  
 Best Local Similarity 73.5%; Pred. No. 1.18e-90;  
 Matches 72; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
  
 Db 20 QVQLQQSGAEVLVPGASVKLSCASGYFTFTSYMMHWVKKQPGQGLWIGRIDPNSGGTNY 79  
 QY 1 QVQLVQSGAEVKKPKASVKVCKASGYFTFTSYMMHWVQAPGQGLMGRIDPDGSDY 60  
  
 Db 80 NEKFKSKATLVDTSSSTAYWQLHSLTSDSNAVYCAR 117  
 QY 61 VEKFKKVTLTADTSSPAYMELSLTSDTAVYCAR 98  
  
 RESULT 12  
 ID HV03\_MOUSE STANDARD; PRT; 120 AA.  
 AC P01747;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN V REGION (36-65).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 83131846.  
 RA SIEKEVITZ M., GEFTER M.L., BRODEUR P., RIBLET R.,  
 RA MARSHAK-ROTHSTEIN A.;  
 RL EUR. J. IMMUNOL. 12:1023-1032(1982).  
 CC -1- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES  
 CC THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF  
 CC THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.  
 CC PIR: A02028; HYMSG7.  
 DR HSP: P01789; 6FAB.  
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA.



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RP  SEQUENCE FROM N.A.
RC  STRAIN-C57BL/6;
RX  MEDLINE; 81234548.
RA  BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA  BALTIMORE D.;
RL  CELL 24:625-637(1981).
CC  -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC  THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR  PIR: A02032; HYMS02.
DR  HSP: P01810; LJHL.
KW  IMMUNOGLOBULIN V REGION; SIGNAL.
FT  SIGNAL 1 19
FT  CHAIN 20 117
FT  DOMAIN 20 49
FT  DOMAIN 50 54
FT  DOMAIN 55 68
FT  DOMAIN 69 85
FT  DOMAIN 86 117
FT  DISULFID 41 115
FT  NON_TER 117 117
SQ  SEQUENCE 117 AA; 12867 MW; 48DD1982 CRC32;

Query Match 59.78; Score 511; DB 1; Length 117;
Best Local Similarity 72.28; Pred. No. 2.30e-88;
Matches 70; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Db 20 HVQLQPGAEVLKPGASVKYSSKASGYTFYSYMHVVKRPGGGLGWIGRIHPSDSDTNY 79
Qy 1 QVLVQSGAEVKRPGASVKYSSKASGYTFEYIMYWRQAPGGLEUMGRIDPEDGSIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKGRATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 VEKFKKVTLTADTSSTAYMELSSLTSDTAVYYCA 97
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (145).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
[1]

RP  SEQUENCE FROM N.A.
RC  STRAIN-C57BL/6;
RX  MEDLINE; 81234548.
RA  BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA  BALTIMORE D.;
RL  CELL 24:625-637(1981).
CC  -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC  THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR  PIR: A02034; HYMS45.
DR  HSP: P01810; LJHL.
KW  IMMUNOGLOBULIN V REGION; SIGNAL.
FT  SIGNAL 1 19
FT  CHAIN 20 117
FT  DOMAIN 20 49
FT  DOMAIN 50 54
FT  DOMAIN 55 68
FT  DOMAIN 69 85
FT  DOMAIN 86 117
FT  NON_TER 117 117
SQ  SEQUENCE 117 AA; 12921 MW; D9B6B000 CRC32;

Query Match 59.08; Score 505; DB 1; Length 117;
Best Local Similarity 71.48; Pred. No. 5.41e-87;
Matches 70; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Db 20 OVQLQPGAEVLKPGASVKISKASGYTFYSYMHVVKRPGGGLGWIGRIHPSDSGTV 79

```

QY 1 QVQLVQSGAEVKPGASVKYSCKASGYTFEYYMWVVRQAPGQGLELMGRIDPDEGSIDY 60  
Db 80 NEKFKSKATLTVDKPSSTAYNQLSSLTSEDSAVYYCAR 117  
QY 61 VERFKKVTLTADTSSSTAYMELSSLTSDDTAVYYCAR 98

Search completed: Thu Jan 14 17:13:28 1999  
Job time : 13 secs.

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 W P E L L  
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 (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:13:47 1999; MasPar time 11.40 Seconds  
 515.642 Million cell updates/sec

Tabular output not generated.

Title: >US-08-477-989B-93  
 Description: (1-118) from US08477989B.pap  
 Perfect Score: 856  
 Sequence: 1 QVQLVQSGAEVKKPGASVKV.....GKFNRYFAYWGQGLTVTVSS 118

Scoring table: PAM 150  
 Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: sprembl6  
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle  
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified  
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 40.641; Variance 74.227; scale 0.548

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	629	73.5	125	4	Q99846 PLATELET MEMBRANE GLYC	3.55e-111
2	617	72.1	118	11	O09199 IGM HEAVY CHAIN (FRAGM	1.59e-108
3	590	68.9	244	4	O00288 SINGLE-CHAIN FV FRAGME	1.72e-102
4	575	67.2	118	11	O09200 IGG HEAVY CHAIN (FRAGM	3.67e-99
5	569	66.5	98	4	O43222 RHEUMATOID FACTOR RF-E	7.86e-98
6	553	64.6	138	11	P70173 OKT3 HEAVY CHAIN VARIA	2.74e-94
7	546	63.8	243	11	O35140 KRTI-CD30 MOAB KI-4 SC	9.66e-93
8	545	63.7	111	11	P37407 TYPE II COLLAGEN ANTIB	1.61e-92
9	531	62.0	152	11	O61250 ANTIGEN, B-CELL RECEPT	1.98e-89
10	526	61.4	123	11	O61218 ANTI-DNA HEAVY CHAIN (	2.50e-88
11	526	61.4	249	11	P97512 SINGLE CHAIN FV ANTIBO	2.50e-88
12	516	60.3	120	11	P97746 MONOCLONAL ANTIBODY ID	3.97e-86
13	512	59.8	116	11	O35529 ANTI-ACID PHOSPHATASE	3.01e-85
14	507	59.2	241	11	P37771 ANTI-CEA 79 SINGLE CHA	3.78e-84
15	504	58.9	98	11	O55113 A6 ANTI-[4-HYDROXY-3-N	1.72e-83
16	503	58.8	98	4	O43220 RHEUMATOID FACTOR RF-I	2.86e-83
17	503	58.8	134	11	O61552 CC49 FAB PRECURSOR (FR	2.86e-83
18	501	58.5	120	11	O35528 ANTI-ACID PHOSPHATASE	7.85e-83
19	489	57.1	125	4	O39825 ANTI-HIV-1 GP120 V3 LO	3.35e-80
20	483	56.4	96	4	O43221 RHEUMATOID FACTOR RF-E	6.89e-79

21	470	54.9	129	4	Q99823 ANTI-HIV-1 GP120 ANTIB	4.77e-76
22	468	54.7	124	4	Q99824 ANTI-HIV-1 GP120 ANTIB	1.30e-73
23	440	51.4	125	11	O54733 MA-15 HEAVY CHAIN (FRA	1.61e-69
24	439	51.3	100	4	O43235 RHEUMATOID FACTOR RF-I	2.65e-69
25	426	48.6	136	4	Q99821 ANTI-HIV-1 GP120 ANTIB	1.73e-66
26	416	48.6	120	4	O92477 ANTI-FOLATE BINDING PR	2.50e-66
27	413	48.2	248	11	O63818 IMMUNOTOXIN MIK-BETA 1	1.11e-63
28	412	48.1	239	4	O43690 ANTI-MPL SCFV (FRAGMEN	1.82e-63
29	412	48.1	240	4	O00289 SINGLE-CHAIN FV FRAGME	1.82e-63
30	400	46.7	119	4	Q15987 RHEUMATOID FACTOR D5 H	6.96e-61
31	398	46.5	244	4	O43689 ANTI-HER3 SCFV (FRAGME	1.87e-60
32	392	45.8	122	4	Q99817 ANTI-SSDNA ANTIBODY HE	3.62e-59
33	383	44.7	137	4	O99670 MONOCLONAL ANTIBODY HE	3.08e-57
34	383	44.7	147	4	Q13667 VH3-IG HEAVY CHAIN VAR	3.08e-57
35	379	44.3	98	4	O43226 RHEUMATOID FACTOR RF-I	2.19e-56
36	369	43.1	119	4	Q15983 RHEUMATOID FACTOR C6 H	2.97e-54
37	367	42.9	117	11	Q61195 ANTI-CARCINOMA EMBRYON	7.92e-54
38	358	41.8	122	4	O99505 HEAVY CHAIN FAB FRAGME	6.47e-52
39	357	41.7	98	4	O43228 RHEUMATOID FACTOR RF-I	1.05e-51
40	355	41.5	96	4	O43224 RHEUMATOID FACTOR RF-I	2.80e-51
41	347	40.5	115	4	O43230 RHEUMATOID FACTOR RF-E	1.38e-49
42	345	40.3	121	11	O70568 SINGLE CHAIN FV (FRAGM	3.66e-49
43	338	39.5	121	4	O15526 HRV FAB 026-VH (FRAGME	1.09e-47
44	337	39.4	96	4	O43227 RHEUMATOID FACTOR RF-I	1.78e-47
45	337	39.4	116	4	Q99515 HEAVY CHAIN FAB FRAGME	1.78e-47

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	125 AA.
ID	Q99846			
AC	Q99846;			
DT	01-MAY-1997 (TREMREL. 03, CREATED)			
DT	01-MAY-1997 (TREMREL. 03, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMREL. 06, LAST ANNOTATION UPDATE)			
DE	PLATELET MEMBRANE GLYCOPROTEIN IB (GP1B) SPECIFIC ANTIBODY (FRAGMENT).			
GN	VI-02.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 91370594.			
RA	HIRAIWA A., NUGENT D.J., MILNER E.C.;			
RL	AUTOIMMUNITY 8:107-113(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	GLAS A.M., MILNER E.C.B.;			
RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; U86522; G1816664;			
DR	PFAM; PF00047; 1g.			
FT	NON_TER 1 1			
FT	NON_TER 125 125			
SQ	SEQUENCE 125 AA; 13722 MW; 8576EE5A CRC32;			

Query Match	73.5%;	Score 629;	DB 4;	Length 125;
Best Local Similarity	73.6%;	Pred. No. 3.55e-111;		
Matches	89;	Conservative 11;	Mismatches 18;	Indels 3; Gaps 2;
Db	1	QVQLVQSGAEVKKPGASVKASGYTFTDYIMHWVRQAPQGLEWMGRINPNSGGTKY 60		
Qy	1	QVQLVQSGAEVKKPGASVKASGYTFTDYIMHWVRQAPQGLEWMGRIDPEDGSIDY 60		
Db	61	AEKFGQRTMTDTSISAVYHLSRLSRDSDTAVYVCARVLRVGNATFAFIWQGTWTVS 120		
Qy	61	VEKFKKKYTLTADTSSSTAYMELSLTSDTAVYVCARG-KFNRYFAY--WGQGLTVTVS 117		
Db	121	S 121		
Qy	118	S 118		

RESULT 2

ID O09199 PRELIMINARY; PRT; 118 AA.  
AC O09199;  
DT 01-JUL-1997 (TREMELREL. 04, CREATED)  
DT 01-JUL-1997 (TREMELREL. 04, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMELREL. 06, LAST ANNOTATION UPDATE)  
DE IGM HEAVY CHAIN (FRAGMENT).  
OS UNKNOWN.  
OC UNCLASSIFIED.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=(NBXNZW) F1 MOUSE; TISSUE=SPLEEN;  
RA PAYELLE-BROGARD B.;  
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; U44924; G1763745;  
DR PFAM; PF00047; ig.  
FT NON\_TER 1  
FT NON\_TER 118  
SQ SEQUENCE 118 AA; 13117 MW; 0983B8C5 CRC32;  
Query Match 72.1%; Score 617; DB 11; Length 118;  
Best Local Similarity 69.5%; Pred. No. 1.69e-108;  
Matches 82; Conservative 19; Mismatches 17; Indels 0; Gaps 0;  
Db 1 QVQLLESPELVPRGSRVKISKASGYTFTDYINNVKORPGQGLEWIGWYVPGSGNTKY 60  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYIMVWVRQAPQGQLELMGRIDPDGGSIDY 60  
Db 61 NEKFKGKATLVDPSSPAYMQLSLTSDSAVYFCARSYTYGYPAYWGQGLTVTVSA 118  
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYVCARGKFNRYFAYWGQGLTVTVSS 118  
RESULT 3  
ID O00288 PRELIMINARY; PRT; 244 AA.  
AC O00288;  
DT 01-JUL-1997 (TREMELREL. 04, CREATED)  
DT 01-JUL-1997 (TREMELREL. 04, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMELREL. 07, LAST ANNOTATION UPDATE)  
DE SINGLE-CHAIN FV FRAGMENT (FRAGMENT).  
OS SCFV.  
GN OS  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA KONTERMANN R.E.; WING M.G.; WINTER G.;  
RL NAT. BIOTECHNOL. 15:629-631(1997).  
DR EMBL; Y13057; E315275;  
DR PFAM; PF00047; ig.  
FT NON\_TER 1  
FT NON\_TER 244  
SQ SEQUENCE 244 AA; 26127 MW; A4CF148B CRC32;  
Query Match 68.9%; Score 590; DB 4; Length 244;  
Best Local Similarity 70.2%; Pred. No. 1.72e-102;  
Matches 85; Conservative 12; Mismatches 21; Indels 3; Gaps 3;  
Db 1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDHYMHVVRQAPQGQLEWMDPNNGDTRF 60  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYIMVWVRQAPQGQLELMGRIDPDGGSIDY 60  
Db 61 AQRPGVTRMTDRTSISAAVNEVSRSLSDDTAVYVCAREGTGSAIYGMVWGQGLTVTVS 120  
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYVCAR-GK-FN-YRFAYWGQGLTVTVS 117  
Db 121 S 121  
QY 118 S 118  
RESULT 4  
ID O09200 PRELIMINARY; PRT; 118 AA.  
AC O09200;

DT 01-JUL-1997 (TREMELREL. 04, CREATED)  
DT 01-JUL-1997 (TREMELREL. 04, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMELREL. 06, LAST ANNOTATION UPDATE)  
DE IGM HEAVY CHAIN (FRAGMENT).  
OS UNKNOWN.  
OC UNCLASSIFIED.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=(NBXNZW) F1 MOUSE; TISSUE=SPLEEN;  
RA PAYELLE-BROGARD B.;  
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; U44925; G1763747;  
DR PFAM; PF00047; ig.  
FT NON\_TER 1  
FT NON\_TER 118  
SQ SEQUENCE 118 AA; 12937 MW; FF570A07 CRC32;  
Query Match 67.2%; Score 575; DB 11; Length 118;  
Best Local Similarity 68.6%; Pred. No. 3.67e-99;  
Matches 81; Conservative 16; Mismatches 21; Indels 0; Gaps 0;  
Db 1 QVQLLESGLAELRPGASVKMSCKASGYTFTSYTMHWKORPGQGLEWIGVINPTSGVTEY 60  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYIMVWVRQAPQGQLELMGRIDPDGGSIDY 60  
Db 61 NQFKDKATLTADSSSTAYMQLSLTSDSAVYVCARSGLGLFDYWGQGLTVTVSS 118  
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYVCARGKFNRYFAYWGQGLTVTVSS 118  
RESULT 5  
ID O43222 PRELIMINARY; PRT; 98 AA.  
AC O43222;  
DT 01-JUN-1998 (TREMELREL. 06, CREATED)  
DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)  
DE RHEUMATOID FACTOR RF-ET7 (FRAGMENT).  
OS OS  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA BORRETTEN M.; NATVIG J.B.; THOMPSON K.M.;  
RL MOL. IMMUNOL. 0:0-0(1997).  
DR EMBL; AF035786; G2665850;  
FT NON\_TER 1  
FT NON\_TER 98  
SQ SEQUENCE 98 AA; 10912 MW; 4F9C1186 CRC32;  
Query Match 66.5%; Score 569; DB 4; Length 98;  
Best Local Similarity 78.6%; Pred. No. 7.86e-98;  
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYIMHWVRQAPQGQLEWGMWINPNSGGTNY 60  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTTEYIMVWVRQAPQGQLELMGRIDPDGGSIDY 60  
Db 61 AOKFGVTRMTDRTSISAYMELSLRSDDTAVYVCAR 98  
QY 61 VEKFKKVTLTADTSSSTAYMELSLTSDTAVYVCAR 98  
RESULT 6  
ID P70173 PRELIMINARY; PRT; 138 AA.  
AC P70173;  
DT 01-FEB-1997 (TREMELREL. 02, CREATED)  
DT 01-FEB-1997 (TREMELREL. 02, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMELREL. 06, LAST ANNOTATION UPDATE)  
DE OKT3 HEAVY CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]

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RX MEDLINE; 97257994.
RA ITO-H.O., UEDA T., HASHIMOTO Y., IMOTO T., KOGA T.;
RL CELL. MOL. LIFE SCI. 53:51-60(1997).
RR ENBL; U69538; G1731665; -
DR PFAM; PF00047; ig.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12444 MW; 6A22312F CRC32;

Query Match 63.7%; Score 545; DB 11; Length 111;
Best Local Similarity 65.8%; Pred. No. 1.61e-92;
Matches 73; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

Db 1 QVQLQSGAEALPGTSVKRMSKASGYTLISYWMNWKQRPQGQLEWIGAINPSNGYTEY 60
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYMYWVRQAPGGQLELMGRIDPDGSDY 60
Db 61 NQKFKRAITLADKSSSTAYMELSSLTSEDSAVYYCAREDYGTHFDYWGQ 111
QY 61 VEKFKKVTLTADTSSSTAYMELSSLTSDTAVYYCARGKF-NYRFAYWGQ 110

RESULT 9
ID Q61250 PRELIMINARY; PRT; 152 AA.
AC Q61250;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ANTIGEN, B-CELL RECEPTOR PRECURSOR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE; 96134009.
RA THIRION S., MORMANS K., HEYLIGEN H., RAUS J., VANDEVYVER C.;
RL IMMUNOGENETICS 43:167-168(1996).
RR ENBL; L43567; G899071; -
DR PFAM; PF00047; ig.
FT SIGNAL.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 152 ANTIGEN, B-CELL RECEPTOR.
SQ SEQUENCE 152 AA; 16517 MW; A83E9253 CRC32;

Query Match 62.08%; Score 531; DB 11; Length 152;
Best Local Similarity 65.08%; Pred. No. 1.98e-89;
Matches 78; Conservative 17; Mismatches 23; Indels 2; Gaps 2;

Db 20 QVQLQSGPELVKPGASVKMSCKASGYKFSYSSVHMVWKQKAGQLEWIGVNPYNDVKY 79
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYMYWVRQAPGGQLELMGRIDPDGSDY 60
Db 80 NGKFKRATLTSKSSSTAYMELSSLTSEDSAVYYCARSAIYDGIAYWGQGTITVSS 139
QY 61 VEKFKKVTLTADTSSSTAYMELSSLTSDTAVYYCARGKF-NYR-FAYWGQTLTVSS 118

RESULT 10
ID Q61218 PRELIMINARY; PRT; 123 AA.
AC Q61218;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ANTI-DNA HEAVY CHAIN (FRAGMENT).
GN J558.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C3H/HEJ-LPR/LPR;
RX MEDLINE; 96134009.
RA WLOCH M.K., ALEXANDER A.L., PIPBEN A.M.M., BISEFSKY D.S.

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 W P S R L H  
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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:15:07 1999; MasPar time 8.09 Seconds

Tabular output not generated.

Title: >US-08-477-989B-93  
 Description: (1-118) from US08477989B.pap  
 Perfect Score: 856  
 Sequence: 1 QVQLVQSGAEYKKPKASVKV.....GKFNRYFAYWGQGLTVVSS 118

Scoring table: PAM 150  
 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: a-geneseq32  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19 20:part20 21:part21 22:part22 23:part23  
 24:part24 25:part25 26:part26 27:part27 28:part28  
 29:part29

Statistics: Mean 30.259; Variance 159.512; scale 0.190

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	750	87.6	140 11	R59084 LO-CD2a VH and leader	4.61e-49
2	739	86.3	163 11	R59089 Protein encoded by re	3.46e-48
3	654	76.4	120 9	R47491 Humanised anti-CD18 A	1.96e-41
4	653	76.3	116 24	W22418 Reshaped human AUK12-	2.35e-41
5	653	76.3	135 6	R29017 pUC-RVH-1220b.	2.35e-41
6	653	76.3	135 6	R29016 pUC-RVH-1220b.	2.35e-41
7	648	75.7	120 25	W37551 Human Ab heavy chain	5.86e-41
8	642	75.0	139 7	R33953 gH1 variable domain.	1.75e-40
9	642	75.0	139 25	W39753 CDR-grafted humanised	1.75e-40
10	638	74.5	120 20	W56825 Humanised M291 antibo	3.63e-40
11	638	74.5	139 28	W36165 Humanised heavy chain	3.63e-40
12	638	74.5	279 20	W50826 Humanised M291 antibo	3.63e-40
13	632	73.8	382 25	W26651 Chimeric receptor hCT	1.08e-39
14	632	73.8	403 25	W26648 Chimeric receptor hCT	1.08e-39
15	632	73.8	473 25	W26647 Chimeric receptor hCT	1.08e-39
16	632	73.8	514 25	W26647 Chimeric receptor hCT	1.08e-39
17	632	73.8	551 25	W26649 Chimeric receptor hCT	1.08e-39
18	632	73.8	692 25	W26650 Chimeric receptor hCT	1.08e-39

19	629	73.5	118 11	R60305 Chimeric anti HIV ant	1.87e-39
20	629	73.5	118 10	R55126 Mouse-human chimeric	1.87e-39
21	627	73.2	117 5	R25732 Humanised VH region o	2.70e-39
22	624	72.9	140 5	R27051 Reshaped Vha425 antib	4.66e-39
23	623	72.8	222 8	R39267 Humanised C4G1 Ig hea	5.59e-39
24	623	72.8	235 8	R39268 Humanised C4G1 Ig hea	5.59e-39
25	623	72.8	449 8	R43339 Completely humanised	5.59e-39
26	621	72.5	139 12	R62679 Cyl148RHB VH region.	8.05e-39
27	617	72.1	118 24	R27528 Heavy chain variable	1.67e-38
28	616	72.0	135 2	R24107 Humanised anti-tac an	2.00e-38
29	615	71.8	117 18	R88716 Mouse antibody heavy	2.40e-38
30	615	71.8	117 10	R59514 Sequence of the matur	2.40e-38
31	615	71.8	119 15	R81331 Human 2*CL antibody h	2.40e-38
32	615	71.8	136 10	R59512 Sequence of the heavy	2.40e-38
33	613	71.6	117 10	R59515 Sequence of the matur	3.45e-38
34	613	71.6	135 2	R06369 Anti-Tac heavy chain	3.45e-38
35	610	71.3	136 29	W47510 Human anti-hepatitis	5.96e-38
36	610	71.3	136 29	W47517 Human anti-hepatitis	5.96e-38
37	610	71.3	136 23	W10584 Anti-hepatitis B heav	5.96e-38
38	610	71.3	136 29	W41054 Human anti-hepatitis	5.96e-38
39	610	71.3	136 2	P70624 Sequence encoded by a	5.96e-38
40	610	71.3	136 23	W16340 Mouse-human chimaeric	5.96e-38
41	610	71.3	136 22	W10239 Chimeric anti-hepatit	5.96e-38
42	610	71.3	139 8	R43689 PBL.3/Humanised heav	5.96e-38
43	610	71.3	139 12	R62678 Cyl148RHA VH region.	5.96e-38
44	609	71.1	119 24	W22425 Humanized alpha-4 int	7.15e-38
45	609	71.1	119 15	R81324 Humanized VLA-4 antib	7.15e-38

ALIGNMENTS

RESULT 1  
 ID R59084 standard; Protein; 140 AA.  
 AC R59084;  
 DE 01-MAY-1995 (first entry)  
 KW LO-CD2a VH and leader sequence from MRC vector hcmv-vllys-kr-neo.  
 KW signal sequence; MRC; chain; variable; constant; antibody;  
 KW monoclonal antibody; MAB; T lymphocyte; null cell; B lymphocyte;  
 KW CD4; CD8; Leu3a; Leu2b; inhibition; immune response; human;  
 KW T cell; activation; proliferation; graft transplantation;  
 KW graft-versus-host disease; autoimmune disease.  
 OS Rattus rattus.  
 FH Key Location/Qualifiers  
 FT peptide 1..22  
 FT protein /note= "MHC vector leader sequence"  
 FT 23..140  
 FT /note= "LoCD2a VH"  
 PN W09420619-A.  
 PD 15-SEP-1994.  
 PF 04-MAR-1994; IB0043.  
 PR 05-MAR-1993; US-027008.  
 PR 09-SEP-1993; US-119032.  
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.  
 PI Bazin H, Latinne D;  
 WP1; 94-303026/37.  
 DR N-PSDB; 071877.  
 DR New anti-CD2 monoclonal antibody - used for inhibiting an immune  
 PT response mediated by T cell activation and proliferation  
 PS Claim 30; Fig 30A; 101pp; English.  
 CC This sequence represents the LO-CD2a heavy chain variable region from  
 CC the antibody LO-CD2a, and the signal sequence from the cell line ATCC HB 11423. It  
 CC is pref. a rat monoclonal antibody and is produced using CD2. This  
 CC antibody, or fragments of it, binds to all T lymphocytes and also to  
 CC null cells but not to B lymphocytes. It binds to all CD4 and CD8  
 CC positive cells as defined by Leu3a and Leu2b antibodies respectively.  
 CC LO-CD2a can be used for inhibiting an immune response in a human patient,  
 CC partic. an immune response mediated by T cell activation and  
 CC proliferation resulting from graft transplantation, graft-versus-  
 CC host disease or autoimmune diseases.  
 SQ Sequence 140 AA;



KW	Monoclonal antibody; MAb; heavy chain; light chain; constant region; variable region; amplification; primer; polymerase chain reaction; PCR; chimera; Ig; immunoglobulin; humanised antibody; leucocyte; integrin. Chimeric: Homo sapiens.
OS	Chimeric: Mus sp.
EP	EP-578515-A.
PN	12-JAN-1994.
PF	24-MAY-1993; 401328.
PP	26-MAY-1992; US-888233.
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.
PI	Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H; WPI: 94-010334/02.
DR	N-P8DB; Q54999.
PT	Humanised monoclonal antibodies prepn. - using comparative model building, by computer database searching
PT	Disclosure, Page 18; 68pp; English.
CC	A humanised monoclonal antibody corresponding to the murine anti-CD18 antibody 60.3 was prepared. The variable (V) region sequences from both the heavy (H) and light (L) chains were determined from cDNA (amplified by PCR), and spliced onto human constant (C) regions, resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was expressed in tissue culture (A8-653 mouse myeloma cells, detected by ELISA), and examined in binding assays. The results from competition and inhibition assays showed that the chimeric Ab was as effective as the murine 60.3 Mab. The deduced murine VH and VL protein sequences were compared to the protein sequence data base, and two human Ig protein sequences were selected to be used as templates. A murine 60.3 Fv was modeled according to the deduced VH and VL protein sequences. Based on the 60.3 Fv model and the two human template sequences selected from the protein data base, a humanised Fv was modeled. Construction of the humanised 60.3 was done by piecing 5 pairs of complementary oligonucleotides together (spanning the entire V region) to form the VH and VL. These were then attached onto vectors containing genes for appropriate C regions to form humanised Ab (IgG1, kappa). The humanised proteins were again expressed in A8.653 cells and binding assays were done. FACS analyses indicated that the humanised Ab recognised cells expressing CD18. About a dozen of the humanised 60.3 Ab master wells were transferred and assayed for Ig.
CC	Sequence 120 AA;
CC	Query Match 76.4%; Score 654; DB 9; Length 120;
CC	Best Local Similarity 75.9%; Pred. No. 1.96e-41;
CC	Matches 91; Conservative 11; Mismatches 16; Indels 2; Gaps 2
Db	1 qvqlvsgaevkpgasvkscasytftdyvmvvrqapggslwmgripdsdethy 60
QY	1 QVQLVSGAEVKPGASVSKASGYTTETYYMYVVRQAPGGSLWGRIDPDGSDY 60
Db	61 nqkfgrvmttdtstymelsslrdsedtavycargrlgscfamdyvqgqltvss 120
QY	61 VEKFKAKVLTADTSSSTAYMELSLSDTAVIYCARG-KF-NRYFAYWQGGLTVTVSS 118
RESULT	4
ID	W22418 standard; Protein; 116 AA.
AC	W22418;
DT	08-DEC-1997 (first entry)
DE	Reshaped human AUK12-20 VH.
KW	Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW	asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW	metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW	transplant rejection; graft versus host disease; nephritis;
KW	atopic dermatitis; psoriasis; myocardial ischaemia;
KW	acute leucocyte mediated lung injury; therapy; AUK12-20.
OS	Chimeric Homo sapiens;
OS	Chimeric synthetic.
FH	Key Location/Qualifiers
FT	region 1..30
FT	/label= FR1
FT	region 31..35
FT	/label= CDRI

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FT region 36..49
FT /label= FR2
FT region 50..66
FT /label= CDR2
FT region 67..98
FT /label= FR3
FT region 99..105
FT /label= CDR3
FT region 106..116
FT /label= FR4
FT WO9718838-A1.
PD 29-MAY-1997.
PF 21-NOV-1996: U18807.
PR 21-NOV-1995: US-561521.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
DR WPI; 97-297879/27.
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
PS Example 6; Page 44; 107pp; English.
CC This polypeptide comprises version 'b', of a reshaped human
CC antibody AUK12-20 VH region. A DNA fragment encoding the
CC polypeptide was subcloned into vector pUC19 for use as a template
CC for PCR amplification and production of version 'a' of a reshaped
CC human 21.6 VH region (see W22413) that can be used in the
CC construction of novel humanised anti-alpha-4 integrin antibodies.
CC Claimed humanised antibodies are useful in the treatment of
CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC bowel disease, rheumatoid arthritis, transplant rejection, graft
CC versus host disease, tumour metastasis, nephritis, atopic
CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC mediated lung injury.
SQ Sequence 116 AA;

Query Match 76.3%; Score 653; DB 24; Length 116;
Best Local Similarity 79.7%; Pred. No. 2.35e-41;
Matches 94; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

Db 1 qvqlvsgaevkpgasvkscasgysftsyihwvraqpggglewgidpfnngtsy 60
QY 1 QVQLVSGAEVKPGASVKVSKRSGYTFTEYIMYWRQAPQGQLELMGRIDPEDGSIDY 60
Db 61 nqkfkgkvtmtdstntaymelsslrsedtavyycargg-n-rfaywgggtlvtvss 116
QY 61 VERFKKKVTLTADTSSTAYMELSSLTSDTAVYVCARGENYRFAYWGQGLTVTVSS 118

RESULT 5
ID R29017 standard; Protein; 135 AA.
AC R29017;
DT 30-MAR-1993 (first entry)
DE pUC-RVh-1220d.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW complementarity determining region; monoclonal; hybridoma; PCR;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 1..19
FT /note= "Leader peptide"
FT region 20..49
FT /label= FR1
FT region 50..54
FT /label= CDR1
FT region 55..68
FT /label= FR2
FT region 69..85
FT /label= CDR2
FT region 86..117
FT /label= FR3
FT region 118..124
FT /label= CDR3
FT region 125..135
FT /label= FR4
PN WO9718838-A1.
PD 29-MAY-1997.
PF 21-NOV-1996: U18807.
PR 21-NOV-1995: US-561521.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
DR WPI; 97-297879/27.
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
PS Example 6; Page 44; 107pp; English.
CC This polypeptide comprises version 'b', of a reshaped human
CC antibody AUK12-20 VH region. A DNA fragment encoding the
CC polypeptide was subcloned into vector pUC19 for use as a template
CC for PCR amplification and production of version 'a' of a reshaped
CC human 21.6 VH region (see W22413) that can be used in the
CC construction of novel humanised anti-alpha-4 integrin antibodies.
CC Claimed humanised antibodies are useful in the treatment of
CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC bowel disease, rheumatoid arthritis, transplant rejection, graft
CC versus host disease, tumour metastasis, nephritis, atopic
CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC mediated lung injury.
SQ Sequence 116 AA;

Query Match 76.3%; Score 653; DB 24; Length 116;
Best Local Similarity 79.7%; Pred. No. 2.35e-41;
Matches 94; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

Db 1 qvqlvsgaevkpgasvkscasgysftsyihwvraqpggglewgidpfnngtsy 60
QY 1 QVQLVSGAEVKPGASVKVSKRSGYTFTEYIMYWRQAPQGQLELMGRIDPEDGSIDY 60
Db 61 nqkfkgkvtmtdstntaymelsslrsedtavyycargg-n-rfaywgggtlvtvss 116
QY 61 VERFKKKVTLTADTSSTAYMELSSLTSDTAVYVCARGENYRFAYWGQGLTVTVSS 118

RESULT 5
ID R29017 standard; Protein; 135 AA.
AC R29017;
DT 30-MAR-1993 (first entry)
DE pUC-RVh-1220d.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW complementarity determining region; monoclonal; hybridoma; PCR;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 1..19
FT /note= "Leader peptide"
FT region 20..49
FT /label= FR1
FT region 50..54
FT /label= CDR1
FT region 55..68
FT /label= FR2
FT region 69..85
FT /label= CDR2
FT region 86..117
FT /label= FR3
FT region 118..124
FT /label= CDR3
FT region 125..135
FT /label= FR4
PN WO9718838-A1.
PD 29-MAY-1997.
PF 21-NOV-1996: U18807.
PR 21-NOV-1995: US-561521.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
DR WPI; 97-297879/27.
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
PS Example 6; Page 44; 107pp; English.
CC This polypeptide comprises version 'b', of a reshaped human
CC antibody AUK12-20 VH region. A DNA fragment encoding the
CC polypeptide was subcloned into vector pUC19 for use as a template
CC for PCR amplification and production of version 'a' of a reshaped
CC human 21.6 VH region (see W22413) that can be used in the
CC construction of novel humanised anti-alpha-4 integrin antibodies.
CC Claimed humanised antibodies are useful in the treatment of
CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC bowel disease, rheumatoid arthritis, transplant rejection, graft
CC versus host disease, tumour metastasis, nephritis, atopic
CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC mediated lung injury.
SQ Sequence 116 AA;

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PN WO9219759-A.
PD 12-NOV-1992.
PF 24-APR-1992: J00544.
PR 25-APR-1991: JP-095476.
PR 19-FEB-1992: JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI; 92-398882/48.
DR N-PSDB; Q31391.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 159-60; 207pp; Japanese.
CC The sequences given in R29016-17 are portions of monoclonal antibodies
CC which were encoded by plasmids contained within the mouse hybridoma,
CC AUK12-20. The DNA encoding the complementarity determining regions
CC (CDR's) was isolated by polymerase chain reaction. These antibodies
CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells
CC were transformed with plasmids containing fragments of the antibody
CC gene which caused the production of the antibody from the hybridoma
CC cell line.
SQ Sequence 135 AA;

Query Match 76.3%; Score 653; DB 6; Length 135;
Best Local Similarity 79.7%; Pred. No. 2.35e-41;
Matches 94; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

Db 20 qvqlvsgaevkpgasvkscasgysftsyihwvraqpggglewgidpfnngtsy 79
QY 1 QVQLVSGAEVKPGASVKVSKRSGYTFTEYIMYWRQAPQGQLELMGRIDPEDGSIDY 60
Db 80 nqkfkgkvtmtdstntaymelsslrsedtavyycargg-n-rfaywgggtlvtvss 135
QY 61 VERFKKKVTLTADTSSTAYMELSSLTSDTAVYVCARGENYRFAYWGQGLTVTVSS 118

RESULT 6
ID R29016 standard; Protein; 135 AA.
AC R29016;
DT 30-MAR-1993 (first entry)
DE pUC-RVh-1220b.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW complementarity determining region; monoclonal; hybridoma; PCR;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 1..19
FT /note= "Leader peptide"
FT region 20..49
FT /label= FR1
FT region 50..54
FT /label= CDR1
FT region 55..68
FT /label= FR2
FT region 69..85
FT /label= CDR2
FT region 86..117
FT /label= FR3
FT region 118..124
FT /label= CDR3
FT region 125..135
FT /label= FR4
PN WO9219759-A.
PD 12-NOV-1992.
PF 24-APR-1992: J00544.
PR 25-APR-1991: JP-095476.
PR 19-FEB-1992: JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI; 92-398882/48.
DR N-PSDB; Q31391.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity

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region      45..54  
FT          /label= CDR1  
FT          69..85  
region      /label= CDR2  
FT          118..128  
FT          /label= CDR3  
PPN         EP-534742-A.  
31-MAR-1993.  
31-MAR-1993.  
31-MAR-1993.  
308680.  
24-SEP-1992;  
PPR         26-SEP-1991; GB-020467.  
PFA        (CLLT ) CELYTECH LTD.  
ADAIR JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;  
Menendez AT, Owens RJ;  
WPI; 93-102837/13.  
N-P5DB; Q38882-89.  
CDR         Anti-human milk fat globule humanised antibodies - useful as  
PT          conjugate for in-vivo diagnosis and therapy of e.g. ovarian or  
PT          breast cancer  
PT          Disclosure; Page 27; 57pp; English.  
CCC         This sequence represents the CDR-grafted heavy chain, gH1. This  
CCC         protein is encoded by the DNA constructed using the oligonucleotides  
CCC         given in Q38882-89. This heavy chain was used in conjunction with a  
CCC         light chain (see also R3954), in the production of a humanised  
CCC         antibody molecule (HAM). At least one of the complementarity  
CCC         determining regions (CDR's) of the variable domain is derived from  
CCC         the mouse monoclonal antibody (MAB) CTM01 and the remaining immuno-  
CCC         globulin-derived parts of the HAM are derived from a human immuno-  
CCC         globulin (or an analogue). The HAM was used for in vivo diagnosis and  
CCC         therapy of carcinomas of ovary, breast, uterus and lung.  
SSQ         Sequence 139 AA;
```

Query Match 75.0%; Score 642; DB 7; Length 139;  
Best Local Similarity 73.3%; Pred. No. 1.75e-40;  
Matches 88; Conservative 14; Mismatches 16; Indels 2; Gaps 1

Ddb 20 qlqlvsgaevkpgsskvsckasgyttfdyyinvmrqpqggglewmgldpgsgntky 79  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
Y 1 QVQLVSGAEVKPGASVKSCKASGYTFEYYMYVRQAPGQGLEMRIDPEDGSIDY 60

Ddb 80 nekfgkrvtitdstntaymellsrsdsatfycarekttyyamdywggtltvtvss 139  
|||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
Y 61 VEKPKKVTLTADTSSTAYMELSLTSDDTAVYYCARGK--FNRYRAYWGQGLTLTVSS 118

### RESULT 9

IID	W29753 standard; Protein; 139 AA.
AC	W29753;
RC	14-JAN-1998 (first entry)
DE	CDR-grafted humanised antibody heavy chain variable region gH1.
KW	Humanised antibody; CDR-grafted antibody; chimeric antibody; CTM01;
KW	complementarity determining region; human milk fat globule; HMFg;
KW	monoclonal antibody; MAB; mouse; cancer; breast cancer;
KW	ovary carcinoma; lung cancer; uterus cancer; diagnosis; therapy.
KW	Chimeric Homo sapiens.
OS	Chimeric Mus musculus.
OS	Chimeric synthetic.
Key	Location/Qualifiers
Region	45..54
FT	/label= CDR1
FT	/note= "Complementarity determining region 1
FT	from CTM01"
Region	69..85
FT	/label= CDR2
FT	/note= "complementarity determining region 2
FT	from CTM01"
Region	118..128
FT	/label= CDR3
FT	/note= "complementarity determining region 3
FT	from CTM01"
Misc-difference 2	/note= "murine residue"
Misc-difference 37	/note= "murine residue"

[illegible]



WO9723613-A2.  
 PD 03-JUL-1997.  
 PF 23-DEC-1996; G03209.  
 PR 21-DEC-1995; GB-026131.  
 PA (CLLT ) CELLTech THERAPEUTICS LTD.  
 PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;  
 DR WPI: 97-351052/32.  
 N-PSDB: T90514.  
 CC New DNA systems for activating cells - comprising DNA coding for a  
 PT chimeric receptor comprising 2 or more different cytoplasmic  
 PT signalling components.  
 PS Disclosure; Fig 9; 90pp; English.  
 CC This protein comprises a chimeric receptor consisting of an scFv  
 CC engineered from anti-CD3 human antibody CTM01 linked to an  
 CC extracellular spacer comprising the human IgG1 hinge, part of the  
 CC extracellular region of human CD28 and 4 amino acid residues, linked  
 CC to the transmembrane and intracellular regions of the human T cell  
 CC receptor zeta chain. It can be expressed in host (e.g. Jurkat)  
 CC cells using a chimeric receptor gene (see T90514) constructed from  
 CC DNA cassettes encoding each component of the receptor. In a  
 CC cell activation process an effector cell is transformed with DNA  
 CC encoding a chimeric receptor containing 2 or more different  
 CC cytoplasmic signalling components. Also claimed is use of DNA  
 CC encoding a recombinant chimeric receptor in a DNA delivery system.  
 CC The DNA delivery systems can be used for the activation of cells to  
 CC provide e.g. an increase in cell proliferation, expression of  
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation  
 CC of cytolytic activity, differentiation or other effector functions,  
 CC antibody secretion, phagocytosis, tumour infiltration and/or  
 CC increased adhesion. They can be used in the treatment of e.g.  
 CC infectious disease, inflammatory disease, cancer, allergic/atopic  
 CC disease, congenital disease, dermatologic disease, neurologic  
 CC disease, transplants and metabolic/idiopathic disease (claimed).  
 CC In particular, they can be used in the treatment of rheumatoid  
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,  
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple  
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host  
 CC disease or diabetes (claimed).  
 SQ Sequence 382 AA;  
 Query Match 73.8%; Score 632; DB 25; Length 382;  
 Best Local Similarity 72.5%; Pred. No. 1.08e-39;  
 Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1;  
 Db 160 qqlvsgaevkpgsvkscasgytfdyinnwrgapggglwlgwldpgsgntky 219  
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYIMYWRQAPGQGLMGRIDPDGSDY 60  
 Db 220 nekfgkgratltvdstntaymelssrdsedtafcarektttyyamydgwgggtlvtvss 279  
 QY 61 VERFKKRVTLTADTSSSTAYMELSSLTSDTAVYICARGK--FNRYFAYWGQGLTVTVSS 118  
 RESULT 14  
 ID W26648 standard; Protein; 403 AA.  
 AC W26648;  
 DE 12-FEB-1998 (first entry)  
 KW Chimeric receptor hCTM01/CD8/CD28.  
 KW Cell activation; chimeric receptor; DNA delivery; CTM01; scFv; CD8;  
 KW CD26; cell proliferation; cytokine; inflammation; effector;  
 KW cell differentiation; antibody secretion; phagocytosis;  
 KW tumour infiltration; adhesion; infection; cancer; allergy;  
 KW rheumatoid arthritis; osteoarthritis; asthma; eczema;  
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;  
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;  
 KW graft versus host disease; human; therapy.  
 OS Chimeric - Homo sapiens.  
 PN WO9723613-A2.  
 PD 03-JUL-1997.  
 PF 23-DEC-1996; G03209.  
 PR 21-DEC-1995; GB-026131.  
 PA (CLLT ) CELLTech THERAPEUTICS LTD.  
 PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;

DR WPI: 97-351052/32.  
 N-PSDB: T90511.  
 CC New DNA systems for activating cells - comprising DNA coding for a  
 PT chimeric receptor comprising 2 or more different cytoplasmic  
 PT signalling components.  
 PS Disclosure; Fig 6; 90pp; English.  
 CC This protein comprises a chimeric receptor consisting of an scFv  
 CC engineered from anti-CD3 human antibody CTM01 linked to an  
 CC extracellular spacer from part of human CD8 hinge, linked to the  
 CC extracellular and intracellular components of human CD28. It can  
 CC be expressed in host cells using a chimeric receptor gene (see  
 CC T90511) constructed from DNA cassettes of each component. In a  
 CC claimed cell activation process an effector cell is transformed with  
 CC DNA encoding a chimeric receptor containing 2 or more different  
 CC cytoplasmic signalling components. Also claimed is use of DNA  
 CC encoding a recombinant chimeric receptor in a DNA delivery system.  
 CC The DNA delivery systems can be used for the activation of cells to  
 CC provide e.g. an increase in cell proliferation, expression of  
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation  
 CC of cytolytic activity, differentiation or other effector functions,  
 CC antibody secretion, phagocytosis, tumour infiltration and/or  
 CC increased adhesion. They can be used in the treatment of e.g.  
 CC infectious disease, inflammatory disease, cancer, allergic/atopic  
 CC disease, congenital disease, dermatologic disease, neurologic  
 CC disease, transplants and metabolic/idiopathic disease (claimed).  
 CC In particular, they can be used in the treatment of rheumatoid  
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,  
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple  
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host  
 CC disease or diabetes (claimed).  
 SQ Sequence 403 AA;  
 Query Match 73.8%; Score 632; DB 25; Length 403;  
 Best Local Similarity 72.5%; Pred. No. 1.08e-39;  
 Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1;  
 Db 160 qqlvsgaevkpgsvkscasgytfdyinnwrgapggglwlgwldpgsgntky 219  
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYIMYWRQAPGQGLMGRIDPDGSDY 60  
 Db 220 nekfgkgratltvdstntaymelssrdsedtafcarektttyyamydgwgggtlvtvss 279  
 QY 61 VERFKKRVTLTADTSSSTAYMELSSLTSDTAVYICARGK--FNRYFAYWGQGLTVTVSS 118  
 RESULT 15  
 ID W26646 standard; Protein; 473 AA.  
 AC W26646;  
 DE 12-FEB-1998 (first entry)  
 KW Chimeric receptor hCTM01/CD8/zeta.  
 KW Cell activation; chimeric receptor; DNA delivery; CTM01; scFv; CD8;  
 KW T cell receptor zeta chain; cell proliferation; cytokine;  
 KW inflammation; effector; cell differentiation; antibody secretion;  
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;  
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;  
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;  
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;  
 KW graft versus host disease; human; therapy.  
 OS Chimeric - Homo sapiens.  
 PN WO9723613-A2.  
 PD 03-JUL-1997.  
 PF 23-DEC-1996; G03209.  
 PR 21-DEC-1995; GB-026131.  
 PA (CLLT ) CELLTech THERAPEUTICS LTD.  
 PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;  
 DR WPI: 97-351052/32.  
 N-PSDB: T90509.  
 CC New DNA systems for activating cells - comprising DNA coding for a  
 PT chimeric receptor comprising 2 or more different cytoplasmic  
 PT signalling components.  
 PS Disclosure; Fig 4; 90pp; English.  
 CC This protein comprises a chimeric receptor consisting of an scFv  
 CC engineered from anti-CD3 human antibody CTM01 linked to an

CC extracellular spacer in the form of part of human CD8 hinge, linked  
CC to the extracellular, transmembrane and intracellular components of  
CC the human T cell receptor zeta chain. It can be expressed in host  
CC cells (e.g. Jurkat) using a chimeric receptor gene (see T90509)  
CC constructed from DNA cassettes of each component. In a claimed  
CC cell activation process an effector cell is transformed with DNA  
CC encoding a chimeric receptor containing 2 or more different  
CC cytoplasmic signalling components. Also claimed is use of DNA  
CC encoding a recombinant chimeric receptor in a DNA delivery system.  
CC The DNA delivery systems can be used for the activation of cells to  
CC provide e.g. an increase in cell proliferation, expression of  
CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation  
CC of cytolytic activity, differentiation or other effector functions,  
CC antibody secretion, phagocytosis, tumour infiltration and/or  
CC increased adhesion. They can be used in the treatment of e.g.  
CC infectious disease, inflammatory disease, cancer, allergic/atopic  
CC disease, congenital disease, dermatologic disease, neurologic  
CC disease, transplants and metabolic/idiopathic disease (claimed).  
CC In particular, they can be used in the treatment of rheumatoid  
CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,  
CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple  
CC sclerosis, organ or tissue transplant rejection, graft-versus-host  
CC disease or diabetes (claimed).  
SQ Sequence 473 AA;

Query Match 73.8%; Score 632; DB 25; Length 473;  
Best Local Similarity 72.5%; Pred. No. 1.08e-39;  
Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1;  
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QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTEYMYWVRQAPGQGLELMDRIDPEDGSIDY 60  
Db 220 nekfkgratlvtstntaymelslrsedtafyfcarektyvyamdywgqgtlvtvss 279  
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QY 61 VEKFKKVTLLPADSSPAYMELSLISDDTAVYICARGK--FNRYFAYWGQGLVTVSS 118

Search completed: Thu Jan 14 17:15:38 1999  
Job time : 31 secs.